

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 13.0223 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-19

Sequence: 1 GLRRLKFRNKIKELKXIG 21

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR 791*
1: p1r1*
2: p1r2*
3: p1r3*
4: p1r4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	171	2 JQ1171	18K lipopolysaccha
2	54	51.9	42	2 S65524	antibacterial prot
3	53	51.0	3411	1 GNMVY	genome polypeptide
4	53	51.0	3411	1 GNMVY	genome polypeptide
5	52	50.0	1163	1 GNMVY	genome polypeptide
6	51.5	49.5	976	2 A97104	Zn-dependent metal
7	51	49.0	241	2 G86355	hypothetical prote
8	50	48.1	162	2 H70314	hypothetical prote
9	50	48.1	166	2 S41731	antibacterial prot
10	50	48.1	173	2 S70521	antibacterial prot
11	50	48.1	213	2 B83979	hypothetical prote
12	50	48.1	213	2 B83979	hypothetical prote
13	49.5	47.6	831	2 S48483	hypothetical prote
14	49.5	47.6	932	2 A75052	cytochrome-c heme
15	49.5	47.6	932	2 F69552	leucyl-tRNA synth
16	49	47.1	153	2 E70356	myoglobin - Balka
17	49	47.1	153	2 E70356	myoglobin - Balka
18	49	47.1	324	2 T07982	probable choline-p
19	49	47.1	324	2 T07982	probable choline-p
20	49	47.1	655	2 S57119	hypothetical prote
21	48	46.2	288	2 JN0466	epimerase - human
22	47.5	45.7	297	2 B90061	hypothetical prote
23	47.5	45.7	297	2 B90061	hypothetical prote
24	47.5	45.7	274	2 B90526	conserved hypochr
25	47.5	45.7	274	2 B90526	conserved hypochr
26	47	45.2	73	2 D64373	hypothetical prote
27	47	45.2	121	2 T03182	hypothetical prote
28	47	45.2	174	2 H70471	conserved hypochr
29	47	45.2	259	2 S57283	conserved hypochr
			705	2 F70475	VacB protein (rib

30	47	45.2	766	2 A75332	probable DNA mima
31	47	45.2	1137	2 G84581	copla-like retroel
32	47	45.2	1233	2 G84581	chromosome segrega
33	46	44.2	153	1 MYBD	myoglobin - Bursai
34	46	44.2	153	1 MYBD	myoglobin - dog (c
35	46	44.2	153	1 MYDG	myoglobin - Africa
36	46	44.2	153	1 MYDGH	myoglobin - Indian
37	46	44.2	153	1 MYELA	myoglobin - bat-ea
38	46	44.2	153	1 MYFXE	myoglobin - Cape f
39	46	44.2	153	1 MYFXE	myoglobin - weasel
40	46	44.2	153	1 MYLEM	myoglobin - gray b
41	46	44.2	153	1 MYSLH	myoglobin [val]at
42	46	44.2	153	1 MYSLH	polypeptide deform
43	46	44.2	305	2 T23829	hypothetical prote
44	46	44.2	305	2 T23829	hypothetical prote
45	46	44.2	329	2 T07981	probable choline-p

ALIGNMENTS

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: *Oryctolagus cuniculus* (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

R/Accession: JQ1171, P80226

R/Barick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171; PMID:91354246; PMID:1883348

A/Molecule type: mRNA

A/Residues: 1-171 <LAR>

A/Experimental source: bone marrow

A/Accession: P80226

A/Molecule type: protein

A/Residues: 135-159, 'QIGQL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F1-29/Domain: signal sequence #status predicted <SIG>

F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAR>

Query Match

Best Local Similarity 100.0%; Score 104; DB 2; Length 171;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLRRLKFRNKIKELKXIG 21

DB 135 GLRRLKFRNKIKELKXIG 155

RESULT 2

S65524

antibacterial protein, 11X - guinea pig (fragment)

C/Species: *Cavia porcellus* (guinea pig)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

R/Accession: S65524

R/Yomogida, S.; Nagaoka, I.; Yamashita, T.

A/Title: Purification of the 11- and 5-kDa antibacterial polypeptides from guinea pig n

A/Reference number: S65524; PMID:8644997

A/Accession: S65524

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-42 <YOM>

A/Cross-references: UNIPROT:Q91X12

Query Match

Best Local Similarity 51.9%; Score 54; DB 2; Length 42;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 65.5223 Seconds

(Without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-19

Perfect score: 104

Sequence: 1 GLKRLRKFNKIKELKXIG 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	171	1	CP18_RABIT
2	55	52.9	153	2	P25230 oryctolagus
3	54	51.9	178	2	082267 pyrobaculum
4	53	51.0	400	2	091X12 cavia porce
5	53	51.0	400	2	089295 yellow feve
6	53	51.0	400	2	089297 yellow feve
7	53	51.0	400	2	089299 yellow feve
8	53	51.0	400	2	089304 yellow feve
9	53	51.0	400	2	089311 yellow feve
10	53	51.0	400	2	089317 yellow feve
11	53	51.0	631	2	07RDG3 plasmodium
12	53	51.0	778	2	P89915 yellow feve
13	53	51.0	778	2	077X62 yellow feve
14	53	51.0	778	2	077X64 yellow feve
15	53	51.0	809	2	09W9B8 yellow feve
16	53	51.0	809	2	06FTT3 yellow feve
17	53	51.0	3411	1	POLG_YEPV1
18	53	51.0	3411	1	POLG_YEPV2
19	53	51.0	3411	2	091857 yellow feve
20	53	51.0	3411	2	098803 yellow feve
21	53	51.0	3411	2	06DVB8 yellow feve
22	53	51.0	3411	2	06X3P1 yellow feve
23	53	51.0	3411	2	06X46 yellow feve
24	53	51.0	3411	2	089275 yellow feve
25	53	51.0	3411	2	089276 yellow feve
26	53	51.0	3411	2	089277 yellow feve
27	53	51.0	3411	2	089278 yellow feve
28	53	51.0	3411	2	09YRV3 yellow feve
29	53	51.0	3411	2	09YRV3 yellow feve
30	53	51.0	3411	2	09YVNI yellow feve
31	53	51.0	3411	2	09YVNI yellow feve
32	52	50.0	249	2	08C804 mus musculi

32	52	50.0	307	2	Q7RLD2	Q7RLD2 plasmodium
33	52	50.0	364	2	Q7RMJ3	Q7RMJ3 plasmodium
34	52	50.0	400	2	089315	089315 yellow feve
35	52	50.0	1163	1	POLG_YEPV8	P29165 yellow feve
36	51.5	49.5	976	2	0971I7	0971I7 clostridium
37	51	49.0	205	2	06FIM8	06F1W8 candida gla
38	51	49.0	228	2	074MC7	074MC7 nanocarchaeu
39	51	49.0	241	2	07G888	07G888 arabidopsis
40	51	49.0	301	2	Q7RBE0	Q7RBE0 plasmodium
41	51	49.0	314	2	Q7RI81	Q7RI81 plasmodium
42	51	49.0	400	2	089308	089308 yellow feve
43	51	49.0	400	2	089309	089309 yellow feve
44	51	49.0	575	2	08EW11	08EW11 mycoplasma
45	50	48.1	113	2	Q7RA52	Q7RA52 plasmodium

ALIGNMENTS

RESULT 1
CP18_RABIT
ID CP18_RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RX MEDLINE=9154246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein."
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN (2)
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity."
RL Infect. Immun. 62:1421-1426(1994).
RN (3)
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity."
RL J. Immunol. 152:231-240(1994).
RN (4)
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tosi A., Scocchi M., Skerlavaj B., Gennaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes."
RL FEBS Lett. 339:108-112(1994).
RN (5)
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes."
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 17.9832 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KMLRRIKRIHIKKYGPVIRIRIIG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR79:*
2: PIR79:*
3: PIR79:*
4: PIR79:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	103	72.5	152	2	S68411	cathelin-related p
2	103	72.5	160	2	S68412	cathelin-related p
3	103	72.5	160	2	S68228	myeloid antimicrob
4	56.5	39.8	152	2	A72385	arginine repressor
5	50	35.2	286	2	D70403	ferredoxin oxidore
6	50	35.2	297	2	H70446	UTP-glucose-1-phos
7	49.5	34.9	617	2	T15104	hypothetical protei
8	49	34.5	266	2	P75119	hypothetical protei
9	49	34.5	363	2	T44564	probable thiamin b
10	49	34.5	429	2	D90428	hypothetical protei
11	49	34.5	988	2	A40628	probable transpos
12	49	34.5	1896	1	RNF2L	DNA-directed RNA p
13	48	33.8	181	2	T15378	hypothetical protei
14	48	33.8	346	2	F69109	conserved hypothet
15	48	33.8	406	2	A71965	hypothetical protei
16	48	33.8	483	2	AE1189	beta-glucosidase h
17	48	33.8	483	2	AP1547	beta-glucosidase h
18	48	33.8	529	2	T48253	myb-like protein -
19	48	33.8	572	2	AC1200	phosphotransferase
20	48	33.8	572	2	A11557	phosphotransferase
21	47.5	33.5	290	2	B89982	hypothetical protei
22	47.5	33.5	456	2	D84651	hypothetical protei
23	47	33.1	143	2	S58584	ribosomal protein
24	47	33.1	171	2	H72405	hypoxanthine phosph
25	47	33.1	181	2	B90246	TATA box binding p
26	47	33.1	213	2	A30302	sodium channel pro
27	47	33.1	247	2	T30008	hypothetical protei
28	47	33.1	295	2	A56595	sodium channel alpi
29	47	33.1	428	2	S35215	sodium channel ptei

30	47	33.1	440	1 T06837	proteolophyllid
31	47	33.1	686	2 T14203	NADH2 dehydrogenas
32	47	33.1	1689	2 S72467	sodium channel pro
33	47	33.1	1784	2 T43167	sodium channel pro
34	47	33.1	1820	2 A33299	sodium channel pro
35	47	33.1	2108	2 S72458	sodium channel pro
36	46.5	32.7	1670	2 T06754	DNA-directed RNA p
37	46	32.4	143	1 R3R211	ribosomal protein
38	46	32.4	240	2 A95327	probable response
39	46	32.4	293	2 B71012	hypothetical prote
40	46	32.4	319	1 S19248	RNA-directed DNA p
41	46	32.4	319	2 C97806	hypothetical prote
42	46	32.4	422	2 A99285	hypothetical prote
43	46	32.4	442	2 S73472	probable thiolphene
44	46	32.4	490	2 S44545	SSH1 protein - yea
45	46	32.4	570	1 C46238	phosphotransferase

ALIGNMENTS

RESULT 1

S68411

Cathelin-related protein 2 precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S68411

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Calguri, D.J.; Huttner, K.M.

A>Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A:Reference number: S68411; MUID:96140581; PMID:8549789

A:Accession: S68411

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-152 <MAH>

A:Cross-references: EMBL:X92757

C:Genetics:

A:Gene: SC5-2

C:Superfamily: cathelin; cystatin homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:14-123/Domain: cystatin homology <CYS>

F:21-123/Domain: propeptide #status predicted <PRO>

F:124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match Best Local Similarity 72.5%; Score 103; DB 2; Length 152; Matches 20; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 KMLRRIKRIHIKKYGPVIRIRIIG 29

DB 124 RGLRLGRKRIAGVKYGPVIRIRIIG 152

RESULT 2

S68412

Cathelin-related protein 1 precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S68412

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Calguri, D.J.; Huttner, K.M.

A>Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A:Reference number: S68411; MUID:96140581; PMID:8549789

A:Accession: S68412

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-160 <MAH>

A:Cross-references: EMBL:X92758

C:Genetics:

A:Gene: SC5-1

C:Superfamily: cathelin; cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:122-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:06 ; Search time 90.4832 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KMLRRIRKIHIIKKXGPTLRIRIRIG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	72.5	160	SCS1_SHEEP	P49928 ovine aries
2	103	72.5	160	SCS2_SHEEP	P49929 ovine aries
3	67	47.2	159	MB28_BOVIN	P54229 bovine taurus
4	57.5	40.5	178	Y005_CORGL	O8nnd4 Corynebacter
5	56.5	39.8	152	ARCR_THEMEA	O9wv19 Thermotoga
6	54.5	38.4	152	O9KKZ0	O9a1h3 Carsonella
7	54	38.0	146	O9A1H3	P56802 Arabidopsis
8	53	37.3	138	R111_ARATH	O7YJUS Calyculantus
9	53	37.3	138	O7YJUS	O81bcs Bacillus
10	53	37.3	196	O81BES	O812c7 Mus musculus
11	53	37.3	108	O8R2C7	O61fj3 Plasmodium
12	53	37.3	413	O6LFRJ3	O7pds0 Plasmodium
13	52.5	37.0	140	O7PDS0	O8f1w3 Corynebacter
14	52.5	37.0	193	Y005_COREF	O91jw2 Arabidopsis
15	52	36.6	255	O91JW2	O8b1w2 Plasmodium
16	52	36.6	1279	O8B1W2	O8u1j1 Pyrococcus
17	51	35.9	267	O8U1J1	O8nph7 Corynebacter
18	51	35.9	295	O8NPH7	O97jy3 Sulfolobus
19	51	35.9	328	O8NPH7	O8h1m5 Micromonas
20	51	35.9	467	O8KXMS	O93xtr Bruguiera
21	51	35.9	756	O93XRS	O6p7a9 Rattus norv
22	51	35.9	953	O6P7A9	O61fh6 Plasmodium
23	51	35.9	6077	O6LFRH6	O61fh6 Plasmodium
24	50	35.2	250	O6LFRH6	O61fh6 Plasmodium
25	50	35.2	286	O672S5	O672S5 Aquifex
26	50	35.2	297	O67602	O67602 Aquifex
27	50	35.2	302	O6EXL6	O66x16 Pseudomonas
28	50	35.2	305	O6BDK5	O8d2k5 Wigglesworth
29	50	35.2	543	O9NUJ2	O9n1j2 Temococcus
30	50	35.2	581	O6EBB6	O6ebdb Campylobact
31	50	35.2	993	O81J59	O81j59 Plasmodium

32	50	35.2	1730	2	O7RNV8	O7rnv8 Plasmodium
33	50	35.2	1903	2	O9U5D6	O9u5d6 Plautia sta
34	50	35.2	2228	2	O7R123	O7r123 Plasmodium
35	49.5	34.9	448	2	O44570	O44570 Caenorhabdi
36	49	34.5	138	1	R111_LORVA	O9bbq3 Lotus japon
37	49	34.5	266	2	O9VON2	O9v0n2 Pyrococcus
38	49	34.5	363	2	O9UWQ2	O9uwq2 Pyrococcus
39	49	34.5	372	2	O7RUL3	O7r1l3 Plasmodium
40	49	34.5	429	2	O97VQ9	O97vg9 Sulfolobus
41	49	34.5	500	1	TF3B_SCHPO	O9p6t0 Schistosach
42	49	34.5	520	2	O8BBH1	O8bbh1 Pseudomonas
43	49	34.5	734	2	O7RGR5	O7rgt5 Plasmodium
44	49	34.5	807	1	HIS8_PHOHL	O7n611 Photorhabdu
45	49	34.5	835	2	O7RNB0	O7rnb0 Plasmodium

ALIGNMENTS

RESULT 1	SCS1_SHEEP	STANDARD	PRT	160 AA.
ID	SCS1_SHEEP			
AC	P49928;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SMAP-29)			
DE	(Myeloid antibacterial peptide SMAP-29).			
OC	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Caprinae; Ovis.			
OK	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow.			
RX	MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;			
RA	Maehoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;			
RT	"Molecular analysis of the sheep cathelin family reveals a novel			
RT	antimicrobial peptide.";			
RT	FEBS Lett. 377:519-522(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Huttner K.M., Maehoney M.M.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Thermostable, broad spectrum, bactericidal agent.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to the cathelicidin family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X92757; CAA63412.1; -			
DR	EMBL; U60600; AAB49715.1; -			
DR	PDB; 1FRY; NMR; A=132-160.			
DR	InterPro: IPR001894; Cathelicidin.			
DR	Pfam; PF00666; Cathelicidins; 1.			
DR	ProDom; PD001838; Cathelicidin; 1.			
DR	PROSITE; PS00946; CATHELICIDINS_1; 1.			
DR	PROSITE; PS00947; CATHELICIDINS_2; 1.			
KW	3D-structure; Antibiotic; Pyrocidone carboxylic acid; Signal.			
FT	SIGNAL	1	29	
FT	PROPEP	30	131	
FT	PEPTIDE	132	160	
FT	MOD_RES	30	30	
FT	DISULFID	86	97	
FT				By similarity.
FT				Cathelin-related peptide SCS.
FT				Pyrocidone carboxylic acid (by
FT				similarity).
FT				By similarity.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 53.0419 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-26

Sequence: 1 KIKKKLXKIGKIGLL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1613378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	52	64.2	170	2	O9GLV5
5	51	63.0	366	2	O8VQ90
6	49	60.5	117	1	PFDB_PYRFU
7	49	60.5	170	1	YF59_METUA
8	49	60.5	171	2	O7IKM5
9	49	60.5	186	2	P70800
10	48	59.3	117	1	PFDB_PYRAB
11	48	59.3	117	1	PFDB_PYRHO
12	48	59.3	270	2	O9NHL6
13	48	59.3	324	2	O42621
14	48	59.3	326	2	O42622
15	48	59.3	326	2	O42622
16	48	59.3	1156	2	O66878
17	47	58.0	68	2	O970H2
18	47	58.0	179	2	O6U1V5
19	47	58.0	179	2	O6U1V7
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21	47	58.0	224	2	O9S0D9
22	47	58.0	244	2	O87584
23	47	58.0	281	2	O8C8N3
24	47	58.0	366	2	O8VQ88
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26	46	56.8	124	2	O9FM18
27	46	56.8	191	2	O44867
28	46	56.8	227	2	O45026
29	46	56.8	284	2	O94B45
30	46	56.8	343	2	O87302
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ALIGNMENTS

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AC	P25230;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	01-MAY-1992 (Rel. 22, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).				
GN	Name=CAP18;				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_Taxid=9986;				
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RP	SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=91354246; PubMed=1883348;				
RA	Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;				
RT	"Complementary DNA sequence of rabbit CAP18 -- a unique				
RL	lipopolysaccharide binding protein.";				
RL	Biochem. Biophys. Res. Commun. 179:170-175(1991).				
RP	(2)				
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RA	MEDLINE=94178952; PubMed=8132348;				
RA	Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I.,				
RT	Wilson D., Yen M.H., Wright S.C., Larrick J.W.;				
RL	"Characterization of a rabbit cationic protein (CAP18) with				
RL	lipopolysaccharide-inhibitory activity.";				
RL	Infect. Immun. 62:1421-1426(1994).				
RP	(3)				
RX	SEQUENCE OF 135-154, AND CHARACTERIZATION.				
RA	MEDLINE=94075827; PubMed=8254193;				
RA	Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,				
RT	Cavallion J.M., Warren H.S., Wright S.C.;				
RL	"A novel granulocyte-derived peptide with lipopolysaccharide-				
RL	neutralizing activity.";				
RL	J. Immunol. 152:231-240(1994).				
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RX	CHARACTERIZATION.				
RA	MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;				
RT	Tosi A., Scocchi M., Skerlavaj B., Gennaro R.;				
RT	"Identification and characterization of a primary antibacterial domain				
RT	in CAP18, a lipopolysaccharide binding protein from rabbit				
RT	leukocytes.";				
RL	FEBS Lett. 339:108-112(1994).				
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RA	MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-0;				
RA	Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F.,				
RT	Huang T.-H.;				
RT	"The solution structure of the active domain of CAP18 -- a				
RT	lipopolysaccharide binding protein from rabbit leukocytes.";				
RL	FEBS Lett. 370:46-52(1995).				

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 / Search time 14.2458 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-24
Perfect score: 75
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	51	68.0	16	3	US-09-322-911-11
7	47	62.7	18	4	US-09-525-269A-10
8	46	61.3	33	5	PCT-US95-12080-4
9	45	61.3	3421	4	US-09-452-638-53
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33	39	52.0	96	4	US-09-732-210-707	Sequence 707, App
34	39	52.0	154	4	US-09-248-796A-27970	Sequence 27970, A
35	39	52.0	166	4	US-09-270-767-38279	Sequence 38279, A
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RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larick, Susan W.
APPLICANT: Wright, James C.
APPLICANT: Hirta, Mshimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

Tue May 3 11:58:24 2005

US-09-642-744d-24.ral

Pl. mail w/ Office Am
Page 2

NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

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QY 1 RKRNRKIKKKKIG 15
DB 7 RKRNRKIKKKKIG 21

RESULT 2 *

US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888

GENERAL INFORMATION:
APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hiraata, Mishinasa

APPLICANT: Ballint, Robert F.

TITLE OF INVENTION: Human Cationic Proteins Having

TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280

FILING DATE: August 1, 1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681

FILING DATE: September 27, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 15325-000920

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURES:

LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

Query Match: 100.0%; Score 75; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRNRKIKKKKIG 15
DB 7 RKRNRKIKKKKIG 21

RESULT 3

US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hiraata, Mishinasa

APPLICANT: Ballint, Robert F.

TITLE OF INVENTION: Human Cationic Proteins Having

TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 29,541

FILING DATE: September 27, 1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 15325-9-1

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681

FILING DATE: September 27, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 15325-000920

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 171 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURES:

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Best Local Similarity 100.0%; Pred. No. 0.002;
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DB 141 RKRNRKIKKKKIG 155

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US-09-332-911-4
; Sequence 4, Application US/09322911
; Patent No. 610388
; GENERAL INFORMATION:
; APPLICANT: Larick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Michimasa
; APPLICANT: Ballint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fites, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULES TYPE: protein
; US-09-332-911-4

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QY 1 RKRFRNKIKKTKKIG 15
Db 141 RKRFRNKIKKTKKIG 155

RESULT 5
US-08-313-681A-11
; Sequence 11, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:

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APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heiln, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-681A-11

Query Match 68.0%; Score 51; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFRNKIKEX 10
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Db 7 RFRNKIKEX 16

* RESULT 6
US-09-322-911-11
Sequence 11, Application US/09322911
Patent No. 610388
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

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Page 4

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 68.0%; Score 51; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKPRNKIKK 10
Db 7 RKPRNKIKK 16

RESULT 7
US-09-525-269A-10
Sequence 10, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbiodical domains from platelet microbiodical
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match 62.7%; Score 47; DB 4; Length 18;
Best Local Similarity 46.7%; Pred. No. 2;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RKPRNKIKKIKTG 15

Db 4 KKWKKKIKKIKTG 18

RESULT 8
PCT-US95-12080-4
Sequence 4, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-12080-4

Query Match 61.3%; Score 46; DB 5; Length 33;
Best Local Similarity 73.3%; Pred. No. 4.8;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RKPRNKIKKIKTG 15
Db 4 RKGRKIKKIKTG 18

RESULT 9
US-09-452-638-53
Sequence 53, Application US/09452638
Patent No. 6696281
GENERAL INFORMATION:
APPLICANT: Chambers, Thomas J.
APPLICANT: Monath, Thomas P.
APPLICANT: Guitraho, Parshad
TITLE OF INVENTION: Chimeric Flavivirus Vaccines
FILE REFERENCE: 06132/033004
CURRENT APPLICATION NUMBER: US/09/452,638
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 09/121,587
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/03894
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: US 09/007,664
PRIOR FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: US 08/807,445
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 3421
TYPE: PRT
ORGANISM: Artificial Sequence

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 17.095 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-20

Sequence: 1 KRLRKPFRKIKKIKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	29	1	US-08-313-681A-7
2	89	100.0	29	3	US-09-322-911-7
3	89	100.0	171	1	US-08-313-681A-4
4	89	100.0	171	3	US-09-322-911-4
5	65	73.0	16	1	US-08-313-681A-11
6	65	73.0	16	3	US-09-322-911-11
7	50	56.2	33	5	PCT-US95-12080-4
8	50	56.2	258	4	US-09-828-4447-13
9	49	55.1	18	4	US-09-525-269A-10
10	49	55.1	326	4	US-09-735-846-25
11	49	55.1	452	4	US-09-889-738-21
12	47	52.8	3421	4	US-07-452-638-53
13	46	51.7	18	1	US-07-725-331-29
14	46	51.7	18	5	PCT-US91-05047-29
15	46	51.7	123	4	US-09-148-545-187
16	46	51.7	123	4	US-09-148-545-243
17	46	51.7	188	4	US-09-695-795A-6
18	46	51.7	329	4	US-09-735-846-24
19	46	51.7	331	4	US-09-735-846-23
20	45	50.6	223	4	US-09-344-624-12
21	45	50.6	269	4	US-09-744-989C-3
22	45	50.6	287	4	US-09-744-989C-1
23	45	50.6	287	4	US-09-744-989C-5
24	45	50.6	429	4	US-09-583-110-4660
25	45	50.6	531	4	US-09-107-433-5016
26	45	50.6	726	4	US-09-253-991A-26767
27	45	50.6	1244	4	US-09-949-016-11702

ALIGNMENTS

28	44	49.4	96	4	US-09-732-210-707	Sequence 707, App
29	44	49.4	103	3	US-09-308-388-1	Sequence 1, Appl
30	44	49.4	187	3	US-08-493-071-16	Sequence 16, Appl
31	44	49.4	236	3	US-08-493-071-15	Sequence 15, Appl
32	44	49.4	277	1	US-08-690-457-5	Sequence 5, Appl
33	44	49.4	277	2	US-08-628-187-5	Sequence 5, Appl
34	44	49.4	277	3	US-08-493-071-3	Sequence 3, Appl
35	44	49.4	287	1	US-08-690-457-4	Sequence 4, Appl
36	44	49.4	287	2	US-08-628-187-4	Sequence 4, Appl
37	44	49.4	287	3	US-08-493-071-2	Sequence 2, Appl
38	44	49.4	288	1	US-08-690-457-3	Sequence 3, Appl
39	44	49.4	288	2	US-08-628-187-3	Sequence 3, Appl
40	44	49.4	288	3	US-08-493-071-1	Sequence 1, Appl
41	43	48.3	18	1	US-07-725-331-24	Sequence 27, Appl
42	43	48.3	18	1	US-07-725-331-27	Sequence 27, Appl
43	43	48.3	18	5	PCT-US91-05047-24	Sequence 24, Appl
44	43	48.3	18	5	PCT-US91-05047-27	Sequence 27, Appl
45	43	48.3	158	4	US-09-107-532A-5475	Sequence 5475, Ap

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Miehlmasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heilin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

Tue May 3 11:58:17 2005

US-09-642-744d-20.1a1

Page 2

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NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 100.0%; Score 89; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKKIKKIG 18
DB 4 KRLRFRNKIKKIKKIG 21

* RESULT 2

US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888

GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Ballint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
NAME/KEY: Region

LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:
NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"

US-09-322-911-7
Query Match 100.0%; Score 89; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKKIKKIG 18
DB 4 KRLRFRNKIKKIKKIG 21

* RESULT 3

US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4

Query Match 100.0%; Score 89; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKKIKKIG 18
DB 138 KRLRFRNKIKKIKKIG 155

RESULT 4
US-09-322-911-4
Sequence 4, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-322-911-4
Query Match 100.0%; Score 89; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRLKRPNKIKKIKIG 18
DB 138 KRLKRPNKIKKIKIG 155
RESULT 5
US-08-313-681A-11
Sequence 11, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:

APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-681A-11
Query Match 73.0%; Score 65; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRLKRPNKIKK 13
DB 4 KRLKRPNKIKK 16
RESULT 6
US-09-322-911-11
Sequence 11, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

Pls. mail if office open.

FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/691,280
 FILING DATE: August 1, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,761
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,765
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06731
 FILING DATE: July 15, 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/313,681
 FILING DATE: September 27, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitch, Renee A.
 REGISTRATION NUMBER: 35,136
 REFERENCE/DOCKET NUMBER: 15325-000920
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-322-911-11

Query Match 73.0%; Score 65; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKER 13
 DB 4 KRLRFRNKIKER 16

RESULT 7
 PCT-US95-12080-4
 Sequence 4, Application PC/TUS9512080
 GENERAL INFORMATION:
 APPLICANT: Children's Medical Center Corporation
 TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Patrea L. Pabst
 STREET: 2800 One Atlantic Center
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/12080
 FILING DATE:
 CLASSIFICATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404)-873-8794
 TELEFAX: (404)-815-8795
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 PCT-US95-12080-4

Query Match 56.2%; Score 50; DB 5; Length 33;
 Best Local Similarity 75.0%; Pred. No. 3.4;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRKFRNKIKER 18
 DB 3 LRKFRNKIKER 18

RESULT 8
 US-09-828-447-13
 Sequence 13, Application US/09828447
 Patent No. 6720477
 GENERAL INFORMATION:
 APPLICANT: COSTA E SILVA, OSWALDO DA
 APPLICANT: BOHNETT, HANS J.
 APPLICANT: VAN THIELEN, NOCHA
 APPLICANT: CHEN, ROUYING
 APPLICANT: ISHITANI, MANABU
 TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
 FILE REFERENCE: 16313-0037
 CURRENT APPLICATION NUMBER: US/09/828,447
 PRIOR FILING DATE: 2001-08-20
 PRIOR APPLICATION NUMBER: 60/196,001
 PRIOR FILING DATE: 2000-04-07
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 13
 LENGTH: 258
 TYPE: PRT
 ORGANISM: Physcomitrella patens
 US-09-828-447-13

Query Match 56.2%; Score 50; DB 4; Length 258;
 Best Local Similarity 47.1%; Pred. No. 22;
 Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKER 17
 DB 83 KRLRFRNKIKER 99

RESULT 9
 US-09-525-269A-10
 Sequence 10, Application US/09525269A
 Patent No. 6743769
 GENERAL INFORMATION:
 APPLICANT: Yeaman, Michael R.
 APPLICANT: Shen, Alexander J.
 TITLE OF INVENTION: Antimicrobial Peptides and Derived
 FILE REFERENCE: 66742-025(HR5614)
 CURRENT APPLICATION NUMBER: US/09/525,269A
 PRIOR FILING DATE: 2000-03-13
 PRIOR APPLICATION NUMBER: US 09/025,319
 PRIOR FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antimicrobial peptide designed in part upon
 OTHER INFORMATION: microbicidal domains from platelet microbial
 OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
 US-09-525-269A-10

Query Match 55.1%; Score 49; DB 4; Length 18;

As mail w/ office ltr

RESULT 2
US-09-322-911-4
Sequence 4, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Latrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Flett, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-322-911-4

Query Match 100.0%; Score 108; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRLRRFRNKKIKKKIGOKI 22
DB 137 RRLRRFRNKKIKKKIGOKI 158

RESULT 3
US-08-313-681A-7
Sequence 7, Application US/08313681A

Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Latrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:
NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 94.4%; Score 102; DB 1; Length 29;
Best Local Similarity 95.5%; Pred. No. 1.5e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRLRRFRNKKIKKKIGOKI 22
DB 3 RRLRRFRNKKIKKKIGOKI 24

RESULT 4
US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Latrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30

Pls. mail w/ official

Tue May 3 11:58:19 2005

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/322,911
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/691,280
 FILING DATE: August 1, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,761
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,765
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06731
 FILING DATE: July 15, 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/313,681
 FILING DATE: September 27, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fiteb, Renee A.
 REGISTRATION NUMBER: 35,136
 REFERENCE/DOCKET NUMBER: 15325-000920
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Region
 LOCATION: 23
 OTHER INFORMATION: /note= "Xaa is Asp or Lys"
 FEATURE:
 NAME/KEY: Region
 LOCATION: 26
 OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
 FEATURE:
 NAME/KEY: Region
 LOCATION: 27
 OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
 US-09-322-911-7
 Query Match 94.4%; Score 102; DB 3; Length 29;
 Best Local Similarity 95.5%; Pred. No. 1.5e-06;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RKRLKPKFKIKKIGOKI 22
 DB 3 RKRLKPKFKIKKIGOKI 24
 RESULT 5
 US-08-313-681A-11
 Sequence 11, Application US/08313681A
 Patent No. 5618675
 GENERAL INFORMATION:

APPLICANT: Larrick, James W.
 APPLICANT: Wright, Susan C.
 APPLICANT: Hirata, Mishimasa
 TITLE OF INVENTION: Human Cationic Proteins Having
 TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/313,681A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Healin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15325-9-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-313-681A-11
 Query Match 64.8%; Score 70; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRLKPKFKIKK 14
 DB 3 RKRLKPKFKIKK 16
 RESULT 6
 US-09-322-911-11
 Sequence 11, Application US/09322911
 Patent No. 610388
 GENERAL INFORMATION:
 APPLICANT: Larrick, James W.
 APPLICANT: Wright, Susan C.
 APPLICANT: Hirata, Mishimasa
 APPLICANT: Balint, Robert F.
 TITLE OF INVENTION: Human Cationic Proteins Having
 TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/322,911

Please mail at office door

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fiteb, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 64.8%; Score 70; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0092; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRLRRFRNRIKEX 14
Db 3 RRLRRFRNRIKEX 16

RESULT 7
PCT-US95-12080-4
Sequence 4, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid

TOPOLOGY: linear
PCT-US95-12080-4

Query Match 59.3%; Score 64; DB 5; Length 33;
Best Local Similarity 78.9%; Pred. No. 0.1;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRKFRNRIKEXIKIGOKI 22
Db 3 LRKGRKIGRKKIKIGOKI 21

RESULT 8
US-09-735-846-25
Sequence 25, Application US/09735846
Patent No. 6730823
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLTRANSFERASE
FILE REFERENCE: BBI419 US NA
CURRENT APPLICATION NUMBER: US/09/735,846
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/170,375
PRIOR FILING DATE: 13 DECEMBER 1999
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 326
TYPE: PRT
ORGANISM: Brassica napus
US-09-735-846-25

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Best Local Similarity 50.0%; Pred. No. 2.7; Mismatches 3; Indels 0; Gaps 0;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RLKFRNRIKEXIKIGOKI 22
Db 198 RLKGRKIGRKKIKIGOKI 217

RESULT 9
US-09-735-846-24
Sequence 24, Application US/09735846
Patent No. 6730823
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLTRANSFERASE
FILE REFERENCE: BBI419 US NA
CURRENT APPLICATION NUMBER: US/09/735,846
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/170,375
PRIOR FILING DATE: 13 DECEMBER 1999
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 329
TYPE: PRT
ORGANISM: Brassica napus
US-09-735-846-24

Query Match 52.8%; Score 57; DB 4; Length 329;
Best Local Similarity 45.0%; Pred. No. 6.6; Mismatches 3; Indels 0; Gaps 0;
Matches 9; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RLKFRNRIKEXIKIGOKI 22
Db 205 RLKGRKIGRKKIKIGOKI 224

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 / Search time 19.9441 seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-19

Perfect score: 104
Sequence: 1 GLEKRLKFRNKKIKKKXIG 21

Scoring table: BLAST62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	104	100.0	171	1 US-08-313-681A-4	Sequence 4, Appl1
4	104	100.0	171	3 US-09-322-911-4	Sequence 4, Appl1
5	80	76.9	16	1 US-08-313-681A-11	Sequence 11, Appl1
6	80	76.9	16	3 US-09-322-911-11	Sequence 11, Appl1
7	53	51.0	3421	4 US-09-452-638-53	Sequence 53, Appl1
8	50	48.1	33	5 PCT-US95-12080-4	Sequence 4, Appl1
9	50	48.1	258	4 US-09-828-447-13	Sequence 13, Appl1
10	49	47.1	18	4 US-09-525-269A-10	Sequence 10, Appl1
11	49	47.1	37	1 US-08-313-681A-6	Sequence 6, Appl1
12	49	47.1	37	3 US-09-322-911-6	Sequence 6, Appl1
13	49	47.1	245	4 US-09-543-681A-6428	Sequence 6428, Ap
14	49	47.1	269	4 US-09-744-989C-3	Sequence 3, Appl1
15	49	47.1	287	4 US-09-744-989C-1	Sequence 1, Appl1
16	49	47.1	287	4 US-09-744-989C-5	Sequence 5, Appl1
17	49	47.1	326	4 US-09-744-989C-5	Sequence 5, Appl1
18	49	47.1	452	4 US-09-889-738-21	Sequence 21, Appl1
19	48	46.2	103	3 US-09-308-388-1	Sequence 1, Appl1
20	48	46.2	236	3 US-08-493-071-15	Sequence 15, Appl1
21	48	46.2	277	1 US-08-690-457-5	Sequence 5, Appl1
22	48	46.2	277	1 US-08-628-187-5	Sequence 5, Appl1
23	48	46.2	277	3 US-08-493-071-3	Sequence 3, Appl1
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25	48	46.2	287	1 US-08-628-187-4	Sequence 4, Appl1
26	48	46.2	287	3 US-08-493-071-2	Sequence 2, Appl1
27	48	46.2	288	1 US-08-690-457-3	Sequence 3, Appl1

28	48	46.2	288	2 US-08-628-187-3	Sequence 3, Appl1
29	48	46.2	288	3 US-08-493-071-1	Sequence 1, Appl1
30	47	45.2	158	4 US-09-107-532A-5475	Sequence 5475, Ap
31	47	45.2	189	4 US-09-134-000C-4590	Sequence 4590, Ap
32	47	45.2	223	4 US-09-344-624-12	Sequence 12, Appl1
33	47	45.2	1244	4 US-09-949-016-11702	Sequence 11702, A
34	46	44.2	18	5 PCT-US91-05047-29	Sequence 29, Appl1
35	46	44.2	123	4 US-02-148-545-187	Sequence 29, Appl1
36	46	44.2	123	4 US-09-148-545-143	Sequence 187, App
37	46	44.2	188	4 US-09-695-795A-6	Sequence 243, App
38	46	44.2	329	4 US-09-735-846-24	Sequence 24, Appl1
39	46	44.2	331	4 US-09-735-846-23	Sequence 23, Appl1
40	46	44.2	413	3 US-08-942-572-2	Sequence 2, Appl1
41	46	44.2	413	3 US-08-614-069-13	Sequence 13, Appl1
42	46	44.2	413	4 US-09-614-069-14	Sequence 14, Appl1
43	46	44.2	413	4 US-09-821-803A-7	Sequence 7, Appl1
44	46	44.2	413	4 US-09-821-803A-8	Sequence 8, Appl1
45	46	44.2	413	4 US-09-821-803A-7	Sequence 8, Appl1

ALIGNMENTS

* RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675

GENERAL INFORMATION:

APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mshimasa

TITLE OF INVENTION: Human Cationic Proteins Having

TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,681A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Healin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15325-9-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURES:

NAME/KEY: Region

LOCATION: 23

OTHER INFORMATION: /note="Xaa is Asp or Lys"

FEATURE:

NAME/KEY: Region

LOCATION: 26

OTHER INFORMATION: /note="Xaa is a Gln or Ile"

FEATURE:

NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 100.0%; Score 104; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRKLRRFRNKKIKKKIG 21
DB 1 GLRKLRRFRNKKIKKKIG 21

RESULT 2
US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888

GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert P.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/691,280

FILING DATE: August 1, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/916,761

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/916,765

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06731

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/313,681

FILING DATE: September 27, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 15325-000920

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"

FEATURE:

NAME/KEY: Region

LOCATION: 26

OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

FEATURE:

NAME/KEY: Region

LOCATION: 27

OTHER INFORMATION: /note= "Xaa is a Gly or Gln"

QY 1 GLRKLRRFRNKKIKKKIG 21
DB 1 GLRKLRRFRNKKIKKKIG 21

RESULT 3
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Knourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-313-681A-4

QY 1 GLRKLRRFRNKKIKKKIG 21
DB 135 GLRKLRRFRNKKIKKKIG 155

Query Match 100.0%; Score 104; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-322-911-4
Sequence 4, Application US/09322911
Patent No. 610388
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-322-911-4

Query Match 100.0%; Score 104; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGRRLRRFRNKKIKKIG 21
DB 135 GGRRLRRFRNKKIKKIG 155

RESULT 3
US-08-313-681A-11
Sequence 11, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:

APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heblin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-681A-11

Query Match 76.9%; Score 80; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGRRLRRFRNKKIKK 16
DB 1 GGRRLRRFRNKKIKK 16

RESULT 6
US-09-322-911-11
Sequence 11, Application US/09322911
Patent No. 610388
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitea, Renee A.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 76.9%; Score 80; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GRRRLRRRNKIKK 16

RESULT 7
US-09-452-638-53
Sequence 53, Application US/09452638
Patent No. 6696281
GENERAL INFORMATION:
APPLICANT: Chambers, Thomas J.
APPLICANT: Monath, Thomas P.
APPLICANT: Gutrahoo, Farshad
TITLE OF INVENTION: Chimeric Flavivirus Vaccines
FILE REFERENCE: 06132/033004
CURRENT APPLICATION NUMBER: US/09/452,638
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 09/121,587
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/03894
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: US 09/007,664
PRIOR FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: US 08/807,445
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 3421
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: derived from yellow fever virus and Japanese
US-09-452-638-53

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Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LRRRLRRRNKIKK 21
Db 16 VRRGVRSISNKKIKK 35

RESULT 8
PCT-US95-12080-4
Sequence 4, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlanta Center
STREET: 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-12080-4

Query Match 48.1%; Score 50; DB 5; Length 33;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 LRRRNKIKK 21
Db 3 LRRGNKIKK 18

RESULT 9
US-09-828-447-13
Sequence 13, Application US/09828447
Patent No. 6720477
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNER, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
APPLICANT: ISHITANI, MANABU
TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
FILE REFERENCE: 16313-0037
CURRENT APPLICATION NUMBER: US/09/828,447
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 258

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 79.8994 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KNLRRIRKIHIIKKYGPILIRITIG 29

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	104	73.2	21	15 US-10-721-839-17	Sequence 17, Appli
5	104	73.2	23	14 US-10-060-102-16	Sequence 16, Appli
6	104	73.2	23	15 US-10-721-839-16	Sequence 16, Appli
7	103	72.5	29	14 US-10-060-102-4	Sequence 4, Appli
8	103	72.5	29	15 US-10-721-839-4	Sequence 4, Appli
9	103	72.5	160	9 US-09-917-340-36	Sequence 36, Appli
10	103	72.5	160	17 US-10-844-837-36	Sequence 36, Appli
11	103	72.5	160	17 US-10-909-119-51	Sequence 51, Appli
12	98	69.0	28	14 US-10-060-102-3	Sequence 3, Appli
13	98	69.0	28	15 US-10-721-839-3	Sequence 3, Appli

14	95	66.9	19	14	US-10-060-102-21	Sequence 21, Appli
15	95	66.9	19	15	US-10-721-839-21	Sequence 21, Appli
16	95	66.9	21	14	US-10-060-102-23	Sequence 23, Appli
17	95	66.9	21	15	US-10-721-839-23	Sequence 23, Appli
18	91	64.1	18	14	US-10-060-102-22	Sequence 22, Appli
19	91	64.1	18	15	US-10-721-839-22	Sequence 22, Appli
20	91	64.1	20	14	US-10-060-102-24	Sequence 24, Appli
21	91	64.1	20	15	US-10-721-839-24	Sequence 24, Appli
22	90	63.4	18	9	US-09-840-009-2	Sequence 2, Appli
23	90	63.4	18	9	US-09-840-009-9	Sequence 9, Appli
24	90	63.4	18	9	US-09-840-009-16	Sequence 16, Appli
25	90	63.4	18	9	US-09-840-009-23	Sequence 23, Appli
26	90	63.4	18	9	US-09-840-009-30	Sequence 30, Appli
27	90	63.4	18	14	US-10-060-102-9	Sequence 9, Appli
28	90	63.4	18	14	US-10-060-102-12	Sequence 12, Appli
29	90	63.4	18	15	US-10-721-839-12	Sequence 12, Appli
30	90	63.4	18	15	US-10-060-102-10	Sequence 10, Appli
31	88	62.0	18	14	US-10-060-102-10	Sequence 10, Appli
32	88	62.0	18	14	US-10-721-839-11	Sequence 11, Appli
33	88	62.0	18	15	US-10-721-839-10	Sequence 10, Appli
34	88	62.0	18	15	US-10-721-839-11	Sequence 11, Appli
35	85	59.9	18	9	US-09-840-009-4	Sequence 4, Appli
36	85	59.9	18	9	US-09-840-009-8	Sequence 8, Appli
37	85	59.9	18	9	US-09-840-009-11	Sequence 11, Appli
38	85	59.9	18	9	US-09-840-009-15	Sequence 15, Appli
39	85	59.9	18	9	US-09-840-009-18	Sequence 18, Appli
40	85	59.9	18	9	US-09-840-009-22	Sequence 22, Appli
41	85	59.9	18	9	US-09-840-009-25	Sequence 25, Appli
42	85	59.9	18	9	US-09-840-009-29	Sequence 29, Appli
43	85	59.9	18	14	US-10-060-102-25	Sequence 25, Appli
44	85	59.9	18	15	US-10-721-839-25	Sequence 25, Appli
45	84	59.2	18	9	US-09-840-009-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-060-102-8
Sequence 8, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINKS, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:03US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 8
LENGTH: 29
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-8

Query Match 100.0%; Score 142; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KNLRRIRKIHIIKKYGPILIRITIG 29

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 27.5419 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KNLRRIRKRIHIKKYGPVLRIRIRIG 29

Scoring tables: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	90	63.4	18	4	US-09-840-009-16
5	90	63.4	18	4	US-09-840-009-23
6	90	63.4	18	4	US-09-840-009-30
7	85	59.9	18	4	US-09-840-009-4
8	85	59.9	18	4	US-09-840-009-8
9	85	59.9	18	4	US-09-840-009-11
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14	85	59.9	18	4	US-09-840-009-29
15	84	59.2	18	4	US-09-840-009-5
16	84	59.2	18	4	US-09-840-009-12
17	84	59.2	18	4	US-09-840-009-19
18	84	59.2	18	4	US-09-840-009-26
19	83	58.5	18	4	US-09-840-009-6
20	83	58.5	18	4	US-09-840-009-7
21	83	58.5	18	4	US-09-840-009-13
22	83	58.5	18	4	US-09-840-009-14
23	83	58.5	18	4	US-09-840-009-20
24	83	58.5	18	4	US-09-840-009-21
25	83	58.5	18	4	US-09-840-009-27
26	83	58.5	18	4	US-09-840-009-28
27	82	57.7	18	4	US-09-840-009-3

28	82	57.7	18	4	US-09-840-009-10	Sequence 10, Appl
29	82	57.7	18	4	US-09-840-009-17	Sequence 17, Appl
30	82	57.7	18	4	US-09-840-009-24	Sequence 24, Appl
31	82	57.7	18	4	US-09-840-009-31	Sequence 31, Appl
32	76	53.5	18	4	US-09-840-009-34	Sequence 34, Appl
33	76	53.5	18	4	US-09-840-009-35	Sequence 35, Appl
34	74	52.1	18	4	US-09-840-009-32	Sequence 32, Appl
35	74	52.1	18	4	US-09-840-009-33	Sequence 33, Appl
36	70	49.3	18	4	US-09-840-009-1	Sequence 1, Appl
37	67	47.2	159	4	US-09-917-340-34	Sequence 34, Appl
38	65	45.8	18	4	US-09-840-009-36	Sequence 36, Appl
39	65	45.8	18	4	US-09-840-009-37	Sequence 37, Appl
40	53.5	37.7	205	3	US-09-134-001C-4766	Sequence 4766, Ap
41	52	36.6	42	4	US-09-785-0598-7	Sequence 7, Appl
42	52	36.6	48	4	US-09-785-0598-8	Sequence 8, Appl
43	51	35.9	167	4	US-09-107-532A-7260	Sequence 7260, Ap
44	50	35.2	36	4	US-09-785-0598-6	Sequence 6, Appl
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ALIGNMENTS

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RESULT 1
US-09-917-340-36
Sequence 36, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnuley, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
PRIOR FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 160
TYPE: PRT
ORGANISM: Ovis aries
US-09-917-340-36
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Best Local Similarity 72.5%; Score 103; DB 4; Length 160;
Matches 20; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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DB 132 RGLRRGRKIAHGKYGKPTVLRIRIRIG 160
RESULT 2
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6493228
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: May 2, 2005, 12:17:55 ; Search time 101.662 Seconds

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110.327 Million cell updates/sec

Title: US-09-642-744D-28

Perfect score: 142

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Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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8	98	63.0	28	4	AAE20867
9	98	63.0	28	5	ABP53270
10	95	66.9	19	5	ABP53288
11	95	66.9	21	5	ABP53290
12	91	64.1	18	5	ABP53289
13	91	64.1	20	5	ABP53291
14	90	63.4	18	4	AAE20865
15	90	63.4	18	4	AAE20865
16	90	63.4	18	5	AAE20882
17	90	63.4	18	5	AAE20875
18	90	63.4	18	5	AAE20854
19	90	63.4	18	5	AAE20861
20	90	63.4	18	5	AAE20868
21	90	63.4	18	5	ABP53276
22	90	63.4	18	5	ABP53279
23	88	62.0	18	4	AAE20854
24	88	62.0	18	5	ABP53278
25	88	62.0	18	5	ABP53277

26	88	62.0	20	4	AAE20853
27	85	59.9	18	5	AAE20870
28	85	59.9	18	5	AAE20860
29	85	59.9	18	5	AAE20881
30	85	59.9	18	5	AAE20867
31	85	59.9	18	5	AAE20874
32	85	59.9	18	5	AAE20863
33	85	59.9	18	5	AAE20877
34	85	59.9	18	5	AAE20856
35	85	59.9	18	5	ABP53292
36	84	59.2	18	5	AAE20864
37	84	59.2	18	5	AAE20871
38	84	59.2	18	5	AAE20878
39	84	59.2	18	5	AAE20857
40	83	58.5	18	5	AAE20872
41	83	58.5	18	5	AAE20873
42	83	58.5	18	5	AAE20858
43	83	58.5	18	5	AAE20866
44	83	58.5	18	5	AAE20879
45	83	58.5	18	5	AAE20865

ALIGNMENTS

RESULT 1
ID AAB70675 standard; peptide; 29 AA.
AC AAB70675;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:28.
XX
KW Ovine; SNAP29; lupine; RCP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (RESC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX
DR WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70668 to AAB70675 represent antimicrobial peptides (1), of which
CC AAB70668 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCP 18 cathelicidin family peptide. (1) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (1) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 / Search time 10.5419 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-26

Perfect score: 81

Sequence: 1 KIKKELKKIKGKIQGL 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 79:*

1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	171	2 JQ1171	18K lipopolysaccha
2	56	69.1	173	2 S70521	cathelin-related p
3	49	60.5	188	1 F64494	conserved hypochet
4	48	59.3	117	1 H71166	hypothetical prote
5	48	59.3	117	2 E75065	hypothetical prote
6	48	59.3	324	2 T07982	probable choline-p
7	48	59.3	326	2 T07983	choline-phosphate
8	48	59.3	1156	2 B70356	chromosome assembl
9	46	56.8	392	2 B85363	hypothetical prote
10	46	56.8	430	2 D70221	conserved hypochet
11	45	55.6	167	2 S68967	antibacterial pept
12	45	55.6	329	2 T07981	probable choline-p
13	45	55.6	331	2 T07980	probable choline-p
14	45	55.6	623	2 D97047	hypothetical prote
15	45	55.6	829	2 T32744	ATP-dependent deox
16	45	55.6	1166	2 A39432	hypoxanthine-guani
17	44	54.3	178	2 H97293	hypothetical prote
18	44	54.3	280	2 C64471	integrinase/recomb
19	44	54.3	387	2 F95130	UDP-N-acetylglucos
20	44	54.3	425	2 H70410	glucose inhibited
21	44	54.3	519	2 T51496	hypothetical prote
22	44	54.3	611	2 B90543	hypothetical prote
23	43	53.1	93	2 C81812	hypothetical prote
24	43	53.1	110	2 B64591	hypothetical prote
25	43	53.1	110	2 A71921	hypothetical prote
26	43	53.1	194	2 G64322	conserved hypochet
27	43	53.1	216	2 F68300	beta-lactamase (EC
28	43	53.1	281	1 PMSAP	hypothetical prote
29	43	53.1	361	2 T25196	hypothetical prote

ALIGNMENTS

30	43	53.1	428	2 C26532	5-enolpyruvylshik
31	43	53.1	953	2 S54478	probable membrane
32	42	51.9	135	2 A29504	hypothetical 16k p
33	42	51.9	173	2 S55150	hypothetical prote
34	42	51.9	183	2 D84473	En/Spm-like transp
35	42	51.9	235	2 F70405	hypothetical prote
36	42	51.9	270	2 H64248	ribosomal protein
37	42	51.9	309	2 F84952	hypothetical prote
38	42	51.9	313	2 A70441	homoserine kinase
39	42	51.9	332	2 H84730	glycerol-3-phospha
40	42	51.9	380	2 F70399	probable phospholi
41	42	51.9	428	1 D71155	hydrogenase expres
42	42	51.9	522	2 C96608	probable methyl-ac
43	42	51.9	629	2 S20516	hypothetical prote
44	42	51.9	712	2 AE2365	dnak-type molecule
45	42	51.9	712	2 AE2365	dnak-type molecule

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

R/Larrick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171; MUID:91354246; PMID:1883348

A/Accession: JQ1171

A/Molecule type: mRNA

A/Residues: 1-171 <LAR>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'QIGQL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F1-29/Domain: signal sequence #status predicted <SIG>

F30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 81; DB 2; Length 171;

Best Local Similarity 100.0%; Pred. NO. 0.00016; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKKELKKIKGKIQGL 17

DB 146 KIKKELKKIKGKIQGL 162

RESULT 2

S70521

cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

A/Accession: S70521

R/Popova, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bel

FEBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521; MUID:96326596; PMID:8706928

A/Accession: S70521

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-References: UNIPROT:P51437; EMBL:X94353; NID:G1177533; PDB:CA64078.1; PID:G11

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 46.2514 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-26

Perfect score: 81

Sequence: 1 KIKKKLKKIGKIGGL 17

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	32	14 US-10-131-433-1	Sequence 1, Appl1
2	81	100.0	37	14 US-10-060-102-5	Sequence 5, Appl1
3	81	100.0	37	15 US-10-721-839-5	Sequence 5, Appl1
4	81	100.0	37	15 US-10-344-709C-15	Sequence 15, Appl1
5	74	91.4	37	16 US-10-344-709C-7	Sequence 2, Appl1
6	74	91.4	31	17 US-10-344-709C-1	Sequence 1, Appl1
7	56	69.1	32	16 US-10-344-709C-1	Sequence 599, App
8	56	69.1	36	17 US-10-470-048B-599	Sequence 1, Appl1
9	56	69.1	39	15 US-10-060-102-1	Sequence 1, Appl1
10	56	69.1	39	15 US-10-721-839-1	Sequence 1, Appl1
11	56	69.1	36	16 US-10-344-709C-5	Sequence 5, Appl1
12	50	61.7	36	14 US-10-269-171A-2	Sequence 2, Appl1
13	49	60.5	39	14 US-10-060-102-2	Sequence 2, Appl1

14	49	60.5	39	15	US-10-721-839-2	Sequence 2, Appl1
15	48	59.3	324	15	US-10-389-566-1171	Sequence 1171, Ap
16	48	59.3	326	14	US-10-233-926-25	Sequence 25, Appl
17	48	59.3	326	15	US-10-389-566-1172	Sequence 1172, Ap
18	48	59.3	1156	15	US-10-369-493-43	Sequence 43, Appl
19	46	56.8	104	15	US-10-424-599-24541	Sequence 24541, A
20	46	56.8	190	15	US-10-424-599-225312	Sequence 225312,
21	46	56.8	194	14	US-10-333-926-6	Sequence 6, Appl1
22	46	56.8	318	15	US-10-389-566-673	Sequence 673, App
23	46	56.8	318	15	US-10-389-566-674	Sequence 674, App
24	46	56.8	363	14	US-10-233-926-20	Sequence 12, Appl
25	45	55.6	37	16	US-10-344-709C-12	Sequence 47315, A
26	45	55.6	157	16	US-10-767-701-47315	Sequence 178781,
27	45	55.6	275	16	US-10-437-963-1174	Sequence 24, Appl
28	45	55.6	329	15	US-10-389-566-1173	Sequence 1173, Ap
29	45	55.6	331	14	US-10-233-926-23	Sequence 23, Appl
30	45	55.6	331	15	US-10-389-566-1173	Sequence 1174, Ap
31	45	55.6	331	15	US-10-389-566-1174	Sequence 51673, A
32	45	55.6	663	15	US-10-282-122A-51673	Sequence 5082, Ap
33	45	55.6	829	15	US-10-369-493-5082	Sequence 148381,
34	44	54.3	60	16	US-10-437-963-148381	Sequence 40325, A
35	44	54.3	199	15	US-10-425-114-40325	Sequence 194227,
36	44	54.3	216	15	US-10-424-599-194227	Sequence 2252, Ap
37	44	54.3	387	17	US-10-472-928-2252	Sequence 184421,
38	44	54.3	477	16	US-10-437-963-184421	Sequence 112025,
39	44	54.3	692	16	US-10-437-963-112025	Sequence 53473, A
40	44	54.3	72	16	US-10-282-122A-53473	Sequence 56766, A
41	43	53.1	318	15	US-10-282-122A-53473	Sequence 225574,
42	43	53.1	79	15	US-10-767-701-56766	Sequence 8, Appl1
43	43	53.1	110	10	US-10-424-599-225574	Sequence 59241, A
44	43	53.1	168	16	US-09-882-227-8	Sequence 230427,
45	43	53.1	274	15	US-10-767-701-59241	

ALIGNMENTS

RESULT 1
US-10-131-433-1
Sequence 1, Application US/10131433
Publication No. US20030054422A1
GENERAL INFORMATION:
APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolyasaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolyasaccharide Immunoassay
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/10/131,433
PRIORITY FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 32
TYPE: PRT
ORGANISM: Lactine
US-10-131-433-1

Query Match 100.0% Score 81; DB 14; Length 32;
Best Local Similarity 100.0% Pred No. 9.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKKKLKKIGKIGGL 17
DB 12 KIKKKLKKIGKIGGL 28

RESULT 2
US-10-060-102-5
Sequence 5, Application US/10060102
Publication No. US2003002829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STABLETON, JACK

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 16.1453 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-26

Sequence: 1 KIKKXKXKIGKXIGLL 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents AA: *
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pdp: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pdp: *
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pdp: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pdp: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	171	1 US-08-313-681A-4	Sequence 4, Appl
2	81	100.0	171	3 US-09-322-911-4	Sequence 4, Appl
3	63	77.8	29	1 US-08-313-681A-7	Sequence 7, Appl
4	63	77.8	29	3 US-09-322-911-7	Sequence 7, Appl
5	56	69.1	33	5 PCT-US95-12080-4	Sequence 4, Appl
6	48	59.3	326	4 US-09-725-846-25	Sequence 25, Appl
7	47	58.0	306	3 US-09-134-001C-4678	Sequence 4678, Ap
8	46	56.8	194	4 US-09-735-846-6	Sequence 6, Appl
9	46	56.8	363	4 US-09-735-846-20	Sequence 20, Appl
10	45	55.6	329	4 US-09-735-846-24	Sequence 24, Appl
11	45	55.6	331	4 US-09-735-846-23	Sequence 23, Appl
12	44	54.3	90	4 US-08-489-039A-11599	Sequence 11599, A
13	44	54.3	434	4 US-09-489-039A-8456	Sequence 8456, Ap
14	43	53.1	281	2 US-08-284-465-6	Sequence 6, Appl
15	43	53.1	428	1 US-08-476-008-42	Sequence 42, Appl
16	43	53.1	428	1 US-08-306-063-42	Sequence 42, Appl
17	43	53.1	428	1 US-08-833-485-42	Sequence 42, Appl
18	43	53.1	428	3 US-09-137-440-42	Sequence 42, Appl
19	43	53.1	1105	4 US-09-540-236-3299	Sequence 3299, Ap
20	42	51.9	952	4 US-09-328-352-5611	Sequence 5611, Ap
21	41.5	51.2	1770	4 US-10-144-198-44	Sequence 44, Appl
22	41.5	51.2	2221	4 US-10-144-198-30	Sequence 30, Appl
23	41	50.6	99	3 US-09-134-001C-3848	Sequence 3848, Ap
24	41	50.6	101	3 US-09-461-637-204	Sequence 204, App
25	41	50.6	161	4 US-09-640-211A-1054	Sequence 1054, Ap
26	41	50.6	390	4 US-09-543-681A-5753	Sequence 5753, Ap
27	41	50.6	450	4 US-09-248-796A-15183	Sequence 15183, A

28	41	50.6	519	3 US-08-397-445D-2	Sequence 2, Appl
29	41	50.6	617	3 US-09-134-001C-4012	Sequence 4012, Ap
30	41	50.6	2710	2 US-08-568-459A-12	Sequence 12, Appl
31	41	50.6	2710	2 US-08-487-826B-12	Sequence 12, Appl
32	41	50.6	2710	3 US-09-210-826B-12	Sequence 12, Appl
33	41	50.6	3060	2 US-08-487-826B-14	Sequence 14, Appl
34	41	50.6	3421	4 US-09-452-638-53	Sequence 53, Appl
35	40.5	50.0	319	4 US-09-328-352-6042	Sequence 6042, Ap
36	40	49.4	23	2 US-08-505-486-60	Sequence 60, Appl
37	40	49.4	23	3 US-08-801-028-60	Sequence 60, Appl
38	40	49.4	23	3 US-09-340-154-60	Sequence 60, Appl
39	40	49.4	23	4 US-09-482-611B-60	Sequence 60, Appl
40	40	49.4	23	5 PCT-US95-09338-60	Sequence 60, Appl
41	40	49.4	23	5 PCT-US95-09338-60	Sequence 60, Appl
42	40	49.4	27	2 US-08-505-486-61	Sequence 61, Appl
43	40	49.4	27	2 US-08-505-486-62	Sequence 62, Appl
44	40	49.4	27	3 US-08-801-028-61	Sequence 61, Appl
45	40	49.4	27	3 US-08-801-028-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 81; DB 1; Length 171;
Best Local Similarity 100.0%; Pred No. 0.00038;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIKKXKXKIGKXIGLL 17
Db 146 KIKKXKXKIGKXIGLL 162

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OM protein - protein search, using ew model

Run on: May 2, 2005, 12:17:55 ; Search time 59.595 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-26

Perfect score: 81

Sequence: 1 KIKKELKIKGKIKGSL 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseqp19808:*
3: geneseqp19908:*
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5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003s:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	17	4 AAB70673	Aab70673 Lupine RC
2	81	100.0	32	3 AAB28486	Aab28486 Rabbit 1i
3	81	100.0	32	8 ADK70761	Adk70761 Rabbit CA
4	81	100.0	37	4 AAB70665	Aab70665 Lupine RC
5	81	100.0	37	5 ABP53272	Abp53272 Sheep nat
6	81	100.0	142	8 ADK70796	Adk70796 Rabbit CA
7	74	91.4	37	5 ABB07711	Abb07711 Antimicro
8	74	91.4	38	4 AAB51193	Aab51193 E. coli A
9	74	91.4	171	5 ABB07703	Abb07703 Rabbit pe
10	73	90.1	15	4 AAB70672	Aab70672 Lupine RC
11	73	90.1	21	4 AAB70670	Aab70670 Lupine RC
12	63	77.8	26	6 AAB34418	Aab34418 Rabbit CA
13	63	77.8	26	6 AAB34419	Aab34419 Rabbit CA
14	63	77.8	26	6 AAB34417	Aab34417 Rabbit CA
15	63	77.8	26	6 AAB34420	Aab34420 Rabbit CA
16	63	77.8	26	6 AAB34419	Aab34419 Rabbit CA
17	63	77.8	26	6 AAB34420	Aab34420 Rabbit CA
18	63	77.8	26	6 AAB34419	Aab34419 Rabbit CA
19	63	77.8	26	6 AAB34420	Aab34420 Rabbit CA
20	62	76.5	22	4 AAB70668	Aab70668 Lupine RC
21	62	76.5	24	6 AAB34416	Aab34416 Rabbit RC
22	62	76.5	24	6 AAB34416	Aab34416 Rabbit RC
23	62	76.5	24	6 AAB34421	Aab34421 Rabbit CA
24	58	71.6	26	6 ADK70764	Adk70764 Rabbit CA
25	56	69.1	31	5 AAO15559	Aao15559 Murine ca

26	56	69.1	32	5 ABB07697	Abb07697 Murine ca
27	56	69.1	33	2 AAR94449	Aar94449 Mouse ant
28	56	69.1	39	5 ABP53268	Abp53268 Mouse nat
29	56	69.1	173	5 ABB07701	Abb07701 Murine ca
30	53	65.4	37	8 ADQ37908	Adq37908 Cathelic
31	52	64.2	37	8 ADQ37919	Adq37919 Monkey RL
32	50	61.7	36	4 AAG66421	Aag66421 Mouse cat
33	50	61.7	36	4 AAU09819	Aau09819 Mouse cat
34	50	61.7	36	5 AAG31966	Aag31966 Mouse cat
35	50	61.7	36	5 AAG31963	Aag31963 Mouse cat
36	50	61.7	36	5 AAU76940	Aau76940 Mouse cat
37	50	61.7	36	6 ABP58358	Abp58358 Mouse cat
38	50	61.7	36	6 ADU51139	Adu51139 Mouse cat
39	49	60.5	39	5 ABP53269	Abp53269 Mouse cat
40	48	59.3	15	4 AAB70671	Aab70671 Murine ca
41	48	59.3	18	4 AAB70667	Aab70667 Murine ca
42	48	59.3	21	4 AAB70666	Aab70666 Lupine RC
43	48	59.3	324	8 ADJ49167	Adj49167 O11-aseoc
44	48	59.3	326	6 ADA06238	Ada06238 Rape chol
45	48	59.3	326	8 ADJ49168	Adj49168 O11-aseoc

ALIGNMENTS

RESULT 1
AAB70673 standard; peptide; 17 AA.
ID AAB70673:
AC AAB70673:
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:26.
XX
XX
XX Ovine: SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
XX bactericidal; antibiotic; antiviral; microbial growth inhibitor;
XX KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX KM Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX OS
XX Oryctolagus cuniculus.
XX OS
XX WO200112668-A1.
XX PN
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-US022781.
XX PR 18-AUG-1999; 99US-0149886P.
XX PA (IOWA) UNIV IOWA RES FOUND.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Tack BE, Mccrory P, Welsh M, Travis SM, Lehrer R;
XX WPI: 2001-234911/24.
XX DR
XX PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX PS Claim 1; Page 103; 137pp; English.
XX CC AAB70648 to AAB70675 represent antimicrobial peptides (1), of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SMP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (1) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (2) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 46.8017 seconds
(without alignments) 164.122 Million cell updates/sec

Title: US-09-642-744D-25

Sequence: 1 KIKKKKKIKGKIQG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	171	1 CP18_RABIT	P25230 Oryctolagus
2	56	76.7	173	1 CRAM_MOUSE	P51437 mus musculu
3	51	69.9	366	2 O8VQ90	O8VQ90 uncultured
4	50	68.5	1123	2 O6S255	O6S255 streptococc
5	49	67.1	170	2 O9GLV5	O9GLV5 macaca mula
6	48	67.1	171	2 O7IKM5	O7IKM5 ratius norv
7	48	65.8	123	2 O9NHL6	O9NHL6 plasmodium
8	48	65.8	270	2 O6FTR2	O6FTR2 candida gla
9	48	65.8	324	2 O42621	O42621 brassica na
10	48	65.8	326	2 O42622	O42622 brassica na
11	47	64.4	68	2 O970H2	O970H2 sulfolobus
12	47	64.4	170	1 YF59_METIA	YF59_METIA
13	47	64.4	179	2 O6U1V5	O6U1V5 methanococ
14	47	64.4	179	2 O6U1V7	O6U1V7 staphylococ
15	47	64.4	224	2 O9S0D9	O9S0D9 borrelia bu
16	47	64.4	244	2 O87584	O87584 staphylococ
17	47	64.4	281	2 O8C9N3	O8C9N3 staphylococ
18	47	64.4	366	2 O8VQ88	O8VQ88 uncultured
19	46	63.0	117	1 PFDB_PYPAB	PFDB_PYPAB
20	46	63.0	284	2 O94B45	O94B45 arabidopsis
21	46	63.0	392	2 O65549	O65549 arabidopsis
22	46	63.0	405	2 O8VYD9	O8VYD9 arabidopsis
23	46	63.0	889	2 O8XWY3	O8XWY3 clostridium
24	46	63.0	1155	2 O66878	O66878 aquifex aeo
25	45	61.6	117	1 PFDB_PYPAB	PFDB_PYPAB
26	45	61.6	117	1 PFDB_PYPAB	PFDB_PYPAB
27	45	61.6	130	2 O6S8U8	O6S8U8 pyrococcus
28	45	61.6	130	2 O8J6C9	O8J6C9 plasmodium
29	45	61.6	172	2 O6TJZ0	O6TJZ0 canis fami
30	45	61.6	183	2 O7VCL9	O7VCL9 prochloroco
31	45	61.6	329	2 O42620	O42620 brassica na

32	45	61.6	331	2 O42619	O42619 brassica na
33	45	61.6	352	2 O74ML2	O74ML2 nanoarchaeu
34	45	61.6	473	2 O9M8K5	O9M8K5 arabidopsis
35	45	61.6	526	2 O649R7	O649R7 uncultured
36	45	61.6	569	2 O9Z886	O9Z886 zea mays (m
37	45	61.6	663	2 O970S8	O970S8 clostridium
38	45	61.6	665	2 O8X162	O8X162 clostridium
39	45	61.6	668	2 O89110	O89110 clostridium
40	45	61.6	3787	2 O81126	O81126 plasmodium
41	44	60.3	56	2 O6WM87	O6WM87 bdellovibri
42	44	60.3	150	2 O8LL71	O8LL71 theobroma c
43	44	60.3	178	2 O97EB1	O97EB1 clostridium
44	44	60.3	191	2 O44867	O44867 borrelia bu
45	44	60.3	227	2 O45026	O45026 borrelia bu

ALIGNMENTS

RESULT 1
CP18_RABIT
ID CP18_RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (rel. 22, Created)
DT 01-MAY-1992 (rel. 22, Last sequence update)
DT 25-OCT-2004 (rel. 45, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RX MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN (2)
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN (3)
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN (4)
RP CHARACTERIZATION.
RX MEDLINE=9418064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tossi A., Scocchi M., Skerlavaj B., Gennaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN (5)
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Loh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 9.30168 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-25

Perfect score: 73

Sequence: 1 KIKKLLKIKGKIQG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	171	2 J01171	18K lipopolysaccha
2	56	76.7	173	2 S70521	cathelin-related p
3	48	65.8	324	2 T07982	probable choline-p
4	48	65.8	326	2 T07983	choline-phosphate
5	47	64.4	188	1 F64494	conserved hypochet
6	46	63.0	392	2 B85363	hypothetical prote
7	45	63.0	1156	2 B70356	chromosome assembl
8	45	61.6	117	1 H71166	hypothetical prote
9	45	61.6	117	2 H75065	hypothetical prote
10	45	61.6	329	2 T07981	probable choline-p
11	45	61.6	331	2 T07980	DNA ligase (NAD de
12	45	61.6	331	2 T07980	probable choline-p
13	44	60.3	663	2 H97047	hypoxanthine-guan
14	44	60.3	178	2 H97293	hypothetical prote
15	44	60.3	280	2 C64471	hypothetical prote
16	44	60.3	387	2 F95130	integrase/recombin
17	44	60.3	430	2 D70221	UDP-N-acetylglucos
18	44	60.3	519	2 T51486	conserved hypochet
19	44	60.3	829	2 T32744	hypothetical prote
20	43	58.9	93	2 C81812	hypothetical prote
21	43	58.9	194	2 G64322	hypothetical prote
22	43	58.9	281	1 PMSAP	beta-lactamase (BC
23	43	58.9	361	2 T25196	hypothetical prote
24	43	58.9	428	2 C26532	5-enolpyruvylshik
25	42	57.5	167	2 S68967	antibacterial pep
26	42	57.5	173	2 S55150	hypothetical prote
27	42	57.5	267	2 T07215	ribosomal protein
28	42	57.5	332	2 H84730	probable phosphol
29	42	57.5	380	2 F70399	hydrogenase expres

30	42	57.5	611	2 E90543	glucose inhibited
31	42	57.5	629	2 S20516	dnak-type molecule
32	42	57.5	1558	2 B71603	RESA-H3 antigen PR
33	41	56.2	138	2 B90125	40S ribosomal prot
34	41	56.2	148	2 A75041	probable glycetol-
35	41	56.2	274	2 C69444	conserved hypochet
36	41	56.2	313	2 A70441	glycerol-3-phosphat
37	41	56.2	369	2 F82333	iron-sulfur cluste
38	41	56.2	515	2 F96700	protein F12A21.9 l
39	41	56.2	517	2 D86804	sensor protein kin
40	41	56.2	558	2 E81037	formate-tetrahydro
41	41	56.2	558	2 E81037	formate-tetrahydro
42	41	56.2	712	2 AE2365	probable formate-t
43	41	56.2	729	2 T15076	dnak-type molecule
44	41	56.2	865	2 D72206	hypothetical prote
45	40.5	55.5	1019	2 F70342	valine-tRNA ligase
					cation efflux syst

ALIGNMENTS

RESULT 1

J01171 18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: J01171; PS0226

R/Larrick, J.W.; Morgan, J.G.; Pailings, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: J01171; M01D:91354246; PMID:1883348

A/Accession: J01171

A/Molecule type: mRNA

A/Residues: 1-171 <LAR>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'QITQQL' <LA2>

A/Note: 157-Aep was also found

C/Superfamily: cathelin; cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 73; DB 2; Length 171;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKKLLKIKGKIQG 15

Db 146 KIKKLLKIKGKIQG 160

RESULT 2

S70521 cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521

R/Popovnev, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fabb, W.E.; Be

FEBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521; M01D:96326596; PMID:8706928

A/Accession: S70521

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-references: UNIPROT:P51437; EMBL:X94353; NID:g1177533; PIDN:CAA64078.1; PID:g1

C/Superfamily: cathelin; cystatin homology

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-144/Domain: propeptide #status predicted <PRO>

F:145-173/Product: cathelin-related protein #status predicted <MAT>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 40.8101 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-25

Perfect score: 73

Sequence: 1 KIKKLUKXIGQKIQG 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubppaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*

8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*

14: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*

15: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*

18: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*

19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*

20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	32	US-10-131-433-1	Sequence 1, Appli
2	73	100.0	37	US-10-060-102-5	Sequence 5, Appli
3	73	100.0	37	US-10-721-839-5	Sequence 5, Appli
4	73	100.0	37	US-10-344-709C-15	Sequence 15, Appli
5	73	100.0	171	US-10-344-709C-7	Sequence 7, Appli
6	56	76.7	31	US-10-399-442A-2	Sequence 2, Appli
7	56	76.7	32	US-10-344-709C-1	Sequence 1, Appli
8	56	76.7	36	US-10-470-048B-599	Sequence 599, App
9	56	76.7	39	US-10-060-102-1	Sequence 1, Appli
10	56	76.7	39	US-10-721-839-1	Sequence 1, Appli
11	56	76.7	173	US-10-344-709C-5	Sequence 5, Appli
12	50	68.5	36	US-10-269-171A-2	Sequence 2, Appli
13	49	67.1	39	US-10-060-102-2	Sequence 2, Appli

14	49	67.1	39	US-10-721-839-2	Sequence 2, Appli
15	48	65.8	324	US-10-389-566-1171	Sequence 1171, Ap
16	48	65.8	326	US-10-233-926-25	Sequence 25, Appli
17	48	65.8	326	US-10-389-566-1172	Sequence 1172, Ap
18	46	63.0	194	US-10-233-926-6	Sequence 6, Appli
19	46	63.0	318	US-10-389-566-673	Sequence 673, App
20	46	63.0	318	US-10-389-566-674	Sequence 674, App
21	46	63.0	363	US-10-233-926-20	Sequence 20, Appli
22	46	63.0	1156	US-10-369-493-43	Sequence 43, Appli
23	45	61.6	157	US-10-767-701-47315	Sequence 47315, A
24	45	61.6	329	US-10-233-926-24	Sequence 24, Appli
25	45	61.6	329	US-10-389-566-1173	Sequence 1173, Ap
26	45	61.6	331	US-10-233-926-23	Sequence 23, Appli
27	45	61.6	331	US-10-389-566-1174	Sequence 1174, Ap
28	45	61.6	663	US-10-282-122A-51673	Sequence 51673, A
29	44	60.3	60	US-10-437-963-148381	Sequence 148381, A
30	44	60.3	387	US-10-472-928-2252	Sequence 2252, Ap
31	44	60.3	477	US-10-437-963-184421	Sequence 184421, A
32	44	60.3	829	US-10-369-493-5082	Sequence 5082, Ap
33	43	58.9	79	US-10-424-599-225574	Sequence 225574, A
34	43	58.9	428	US-09-661-696-42	Sequence 42, Appli
35	43	58.9	9	US-09-664-099A-42	Sequence 42, Appli
36	43	58.9	428	US-10-369-493-23174	Sequence 23174, A
37	43	58.9	644	US-10-437-963-204425	Sequence 204425, A
38	43	58.9	1094	US-10-282-122A-63383	Sequence 63383, A
39	42	57.5	35	US-10-205-150-1	Sequence 1, Appli
40	42	57.5	37	US-10-344-709C-12	Sequence 12, Appli
41	42	57.5	139	US-10-425-114-40325	Sequence 40325, A
42	42	57.5	216	US-10-424-599-194227	Sequence 194227, A
43	42	57.5	216	US-10-424-599-230427	Sequence 230427, A
44	42	57.5	275	US-10-437-963-178781	Sequence 178781, A
45	42	57.5	304	US-10-425-114-41429	Sequence 41429, A

ALIGNMENTS

RESULT 1

US-10-131-433-1

Sequence 1, Application US/10111433

Publication No. US2003005442A1

GENERAL INFORMATION:

APPLICANT: UNILEVER, PLC

TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device

FILE REFERENCE: Lipopolysaccharide Immunoassay

CURRENT APPLICATION NUMBER: US/10/131,433

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US/09/545,180

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 32

TYPE: PRT

ORGANISM: Lاپine

US-10-131-433-1

Query Match 100.0%, Score 73, DB 14, Length 32,

Best Local Similarity 100.0%, Pred. No. 0.00095,

Matches 15, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 KIKKLUKXIGQKIQG 15

DB 12 KIKKLUKXIGQKIQG 26

RESULT 2

US-10-060-102-5

Sequence 5, Application US/10060102

Publication No. US20030022629A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STAPLETON, JACK

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 14.2458 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-25

Sequence: 1 KIRKJLKKIKGKIQG 15

Scoring table:

BLOSUM62

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	171	1	US-08-313-681A-4
2	73	100.0	171	3	US-09-322-911-4
3	61	83.6	29	1	US-08-313-681A-7
4	61	83.6	29	3	US-09-322-911-7
5	56	76.7	33	5	PCT-US95-12080-4
6	48	65.8	326	4	US-09-735-846-25
7	47	64.4	306	3	US-09-134-001C-4678
8	46	63.0	194	4	US-09-735-846-6
9	46	63.0	363	4	US-09-735-846-20
10	45	61.6	329	4	US-09-735-846-24
11	45	61.6	331	4	US-09-735-846-23
12	44	60.3	434	4	US-09-489-039A-8456
13	43	58.9	281	2	US-08-476-008-42
14	43	58.9	428	1	US-08-306-063-42
15	43	58.9	428	1	US-08-833-485-42
16	43	58.9	428	1	US-09-137-440-42
17	43	58.9	428	3	US-09-540-236-3299
18	43	58.9	1105	4	US-09-543-681A-5753
19	42	57.5	952	4	US-09-489-039A-11599
20	41	56.2	90	4	US-09-540-236-3299
21	41	56.2	390	4	US-09-543-681A-5753
22	40.5	55.5	1770	4	US-10-144-198-44
23	40.5	55.5	2221	2	US-10-144-198-30
24	40	54.8	23	2	US-08-505-486-60
25	40	54.8	23	3	US-08-801-028-60
26	40	54.8	23	3	US-09-340-154-60
27	40	54.8	23	4	US-09-482-611B-60

28	40	54.8	23	5	PCT-US95-09338-60	Sequence 60, Appl
29	40	54.8	23	5	PCT-US95-09339-60	Sequence 60, Appl
30	40	54.8	27	2	US-08-505-486-61	Sequence 62, Appl
31	40	54.8	27	2	US-08-505-486-62	Sequence 62, Appl
32	40	54.8	27	3	US-08-801-028-62	Sequence 62, Appl
33	40	54.8	27	3	US-08-801-028-61	Sequence 62, Appl
34	40	54.8	27	3	US-09-340-154-61	Sequence 62, Appl
35	40	54.8	27	3	US-09-340-154-62	Sequence 62, Appl
36	40	54.8	27	4	US-09-482-611B-61	Sequence 62, Appl
37	40	54.8	27	4	US-09-482-611B-62	Sequence 62, Appl
38	40	54.8	27	5	PCT-US95-09338-61	Sequence 62, Appl
39	40	54.8	27	5	PCT-US95-09338-62	Sequence 62, Appl
40	40	54.8	27	5	PCT-US95-09339-61	Sequence 62, Appl
41	40	54.8	27	5	PCT-US95-09339-62	Sequence 62, Appl
42	40	54.8	28	1	US-08-182-175A-4	Sequence 4, Appl
43	40	54.8	28	5	PCT-US92-06412-4	Sequence 4, Appl
44	40	54.8	150	4	US-09-732-210-1354	Sequence 1354, Ap
45	40	54.8	150	4	US-09-732-210-1361	Sequence 1361, Ap

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mitsuhiro
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313, 681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 73; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 KIRKJLKKIKGKIQG 15
146 KIRKJLKKIKGKIQG 160

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 52.5838 Seconds

(Without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-25

Sequence: 1 KIKKELKIKGKIQG 15

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_16Dec04:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20018:*
6: geneseqp20028:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	15	4 AAB70672	Aab70672 Lupine RC
2	73	100.0	17	4 AAB70673	Aab70673 Lupine RC
3	73	100.0	21	4 AAB70670	Aab70670 Lupine RC
4	73	100.0	32	3 AAB28486	Aab28486 Rabbit 11
5	73	100.0	32	8 ADK70761	Adk70761 Rabbit CA
6	73	100.0	37	4 AAB70665	Aab70665 Lupine RC
7	73	100.0	37	5 AAB807711	Abb07711 Antimicro
8	73	100.0	37	5 ABP53272	Abp53272 Sheep nat
9	73	100.0	38	4 AAB51193	Abd51193 E. coli A
10	73	100.0	142	8 ADK70796	Adk70796 Rabbit CA
11	73	100.0	171	5 AAB07703	Abb07703 Rabbit pe
12	63	86.3	26	6 AAB34418	Aae34418 Rabbit CA
13	63	86.3	26	6 AAB34417	Aae34417 Rabbit CA
14	63	86.3	26	6 AAB34419	Aae34419 Rabbit CA
15	63	86.3	26	6 AAB34420	Aae34420 Rabbit CA
16	63	86.3	26	8 ADK70762	Adk70762 Rabbit CA
17	62	84.9	19	4 AAB70669	Aab70669 Lupine RC
18	62	84.9	22	4 AAB70668	Aab70668 Lupine RC
19	62	84.9	24	6 AAB34416	Aae34416 Rabbit RC
20	62	84.9	24	8 ADK70763	Adk70763 Rabbit CA
21	62	84.9	26	6 AAB34421	Aae34421 Rabbit CA
22	61	83.6	29	2 AAB45671	Aab45671 N terminu
23	61	83.6	29	3 AAB07903	Adk70764 Rabbit CA
24	58	79.5	24	8 ADK70764	Aad07903 Putative
25	56	76.7	31	5 AAO15559	Aad07903 Putative

26	56	76.7	32	5 ABB07697	Abb07697 Murine ca
27	56	76.7	33	2 AAR94449	Aar94449 Mouse ant
28	56	76.7	39	5 ABP53268	Abp53268 Mouse nat
29	56	76.7	173	5 ABB07701	Abb07701 Murine ca
30	50	68.5	36	4 AAG66421	Aag66421 Mouse cat
31	50	68.5	36	5 AAU09819	Aau09819 Mouse cat
32	50	68.5	36	5 ABG31966	Abg31966 Mouse cat
33	50	68.5	36	5 AAB70663	Aab70663 Mouse cat
34	50	68.5	36	5 AAU76940	Aau76940 Mouse cat
35	50	68.5	36	5 ABP58358	Abp58358 Mouse cat
36	50	68.5	36	8 ADJ51139	Adj51139 Mouse cat
37	49	67.1	37	8 ADQ37919	Adq37919 Monkey RL
38	49	67.1	37	8 ADQ37908	Adq37908 Cathelici
39	49	67.1	39	5 ABP53269	Abp53269 Mouse nat
40	48	65.8	15	4 AAB70671	Aab70671 Lupine RC
41	48	65.8	18	4 AAB70667	Aab70667 Lupine RC
42	48	65.8	21	4 AAB70666	Aab70666 Lupine RC
43	48	65.8	324	8 ADJ49167	Adj49167 OLI-asso
44	48	65.8	326	6 ADA06238	Ada06238 Rape chol
45	48	65.8	326	8 ADJ49168	Adj49168 OLI-asso

ALIGNMENTS

RESULT 1
AAB70672
ID AAB70672 standard; peptide; 15 AA.
XX
AC AAB70672:
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:25.
XX
KW Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryctolagus cuniculus.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES POUND.
XX
RE (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccrery P, Welsh M, Travis SM, Lehrer R;
XX
DR WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (1), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (1) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (1) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth. For inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 46.8017 Seconds
(without alignments) 164.122 Million cell updates/sec

Title: US-09-642-744d-24

Perfect score: 75

Sequence: 1 RKFRNKIKKIKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprotc.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	171	1	CP18 RABIT
2	48	64.0	361	2	P25230 oryctolagus
3	48	64.0	439	2	O978N0 thermophilus
4	48	64.0	497	2	O53589 staphylococ
5	48	64.0	497	2	O8NT03 staphylococ
6	48	64.0	497	2	O99R73 staphylococ
7	48	64.0	497	2	O7A3D9 staphylococ
8	48	64.0	497	2	O6G6B0 staphylococ
9	47	62.7	1321	2	O6G6B5 staphylococ
10	46	61.3	169	1	DEP1_VIBCH
11	46	61.3	173	1	GRAM_MOUSE
12	46	61.3	321	2	O7R9Y0
13	46	61.3	400	2	O89295
14	46	61.3	400	2	O89297
15	46	61.3	400	2	O89299
16	46	61.3	400	2	O89304
17	46	61.3	400	2	O89311
18	46	61.3	400	2	O89315
19	46	61.3	400	2	O89317
20	46	61.3	598	2	O48537
21	46	61.3	778	2	P89915
22	46	61.3	778	2	O77X62
23	46	61.3	778	2	O77X64
24	46	61.3	778	2	O9W9B8
25	46	61.3	1111	1	Y0EP_HAEIN
26	46	61.3	1163	1	POLG_YEYF8
27	46	61.3	1280	2	O6CVH7
28	46	61.3	3411	1	POLG_YEYV1
29	46	61.3	3411	1	POLG_YEYV2
30	46	61.3	3411	1	O91857
31	46	61.3	3411	2	O98803
32	46	61.3	3411	2	O98803

32	46	61.3	3411	2	O6DV88	O6DV88 yellow feve
33	46	61.3	3411	2	O6DJPI	O6DJPI yellow feve
34	46	61.3	3411	2	O6PX46	O6PX46 yellow feve
35	46	61.3	3411	2	O89275	O89275 yellow feve
36	46	61.3	3411	2	O89276	O89276 yellow feve
37	46	61.3	3411	2	O89277	O89277 yellow feve
38	46	61.3	3411	2	O89278	O89278 yellow feve
39	46	61.3	3411	2	O9YRV3	O9YRV3 yellow feve
40	46	61.3	3411	2	O9YVNO	O9YVNO yellow feve
41	46	61.3	3411	2	O9YVNO	O9YVNO yellow feve
42	46	61.3	3411	2	O9YVNO	O9YVNO yellow feve
43	45	60.0	142	2	O6E881	O6E881 aquifex aeo
44	45	60.0	166	1	MP36_PIG	P49931 sue scrofa
45	45	60.0	174	2	O9ZVE7	O9ZVE7 arabidopsis

ALIGNMENTS

RESULT 1
CP18_RABIT
ID CP18_RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus;
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RX MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN [3]
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tossi A., Scocchi M., Skerlavaj B., Gemmaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 9.30168 Seconds
(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-24

Perfect score: 75

Sequence: 1 RKFNNKIKKKKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*
2: PIR1.*
3: PIR2.*
4: PIR3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	171	2 JQ1171	18k lipopolysaccha
2	48	64.0	497	2 E90061	hypothetical prote
3	46	61.3	169	2 A82373	polypeptide deform
4	46	61.3	173	2 S70521	cathelin-related p
5	46	61.3	1163	1 GNMVY8	genome polyprotein
6	46	61.3	3411	1 GNMVY	genome polyprotein
7	46	61.3	3411	1 GNMVY	genome polyprotein
8	45	60.0	142	2 E70356	hypothetical prote
9	45	60.0	166	2 S41731	antibacterial prote
10	45	60.0	174	2 F84426	hypothetical prote
11	45	60.0	522	2 A95059	hypothetical prote
12	45	60.0	522	2 A95059	hypothetical prote
13	44	58.7	109	2 H97927	type 1 site-specif
14	44	58.7	109	2 H97927	hypothetical prote
15	43.5	58.0	274	2 T24111	hypothetical prote
16	43	57.3	119	2 C90351	hypothetical prote
17	43	57.3	293	2 T04951	conserved hypotet
18	43	57.3	356	2 F64383	hypothetical prote
19	43	57.3	392	2 D96770	hypothetical prote
20	43	57.3	573	2 D90202	hypothetical prote
21	43	57.3	1631	1 SAZOK1	methionyl-tRNA syn
22	43	57.3	1639	2 S05603	major mezozone su
23	43	57.3	1640	2 A24594	probable major su
24	42	56.0	175	2 A64330	hypothetical prote
25	42	56.0	358	2 D95041	hypothetical prote
26	42	56.0	414	2 H70219	hypothetical prote
27	42	56.0	425	2 C97035	uncharacterized pr
28	42	56.0	476	2 D71108	cysteine-tRNA lig
29	42	56.0	524	1 S60406	hypothetical prote

30	42	56.0	2038	2 A43742	female sterile hom
31	41	54.7	167	2 S25360	signal recognition
32	41	54.7	308	2 D64328	hypothetical prote
33	41	54.7	325	2 D81369	hypothetical prote
34	41	54.7	558	2 A64515	type I restriction
35	41	54.7	561	2 T41176	hypothetical prote
36	41	54.7	588	2 T45539	moed protein limpo
37	41	54.7	647	2 E64170	ABC-type transport
38	41	54.7	831	2 S44843	K06H7.3 protein -
39	41	54.7	851	2 T31520	hypothetical prote
40	40	53.3	96	2 F72228	ribosomal protein
41	40	53.3	127	2 A64466	hypothetical prote
42	40	53.3	133	2 E86796	arsenate reductase
43	40	53.3	176	2 E89519	conserved hypotet
44	40	53.3	233	2 S70531	bbk2.11 protein pr
45	40	53.3	241	2 G86355	hypothetical prote

ALIGNMENTS

RESULT 1
JQ1171
18k lipopolysaccharide-binding protein precursor - rabbit
N:Alternate names: 18k cationic protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C/Accession: JQ1171, PS0226
R:Latrick, J.W.; Morgan, J.G.; Palings, I.; Hixara, M.; Yen, M.H.
Biochem. Biophys. Res. Commun. 179, 170-175, 1991
A>Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide bindin
A:Reference number: JQ1171, MUID:91354246, PMID:1863348
A:Accession: JQ1171
A:Molecule type: mRNA
A:Residues: 1-171 <LAR>
A:Experimental source: bone marrow
A:Accession: PS0226
A:Molecule type: Protein
A:Residues: 135-159, 'OIGQL' <LA2>
A>Note: 157-asp was also found
C:Superfamily: cathelin; cystatin homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-171/Product: 18k lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 75; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKFNNKIKKKKIG 15
Db 141 RKFNNKIKKKKIG 155

RESULT 2
E90061
hypothetical protein SA2351 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: E90061
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shib, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsesu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E90061
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <KUR>
A:Cross-references: UNIPROT:Q99R73; GB:BA000018; PID:g13702514; PIDN:BA843655.1; GSPDB:
A:Experimental source: strain N315
C/Genetic:
A:Gene: SA2351

run on: May 2, 2005, 13:03:56 ; Search time 40.8101 Seconds
(without alignment)

122.435 Million cell updates/sec

Title:	US-09-642-744D-24
Perfect Score:	75

Sequence: 1 RKFRNKIKEKLKIG 15

Scoring table:

Supp 10:00, Gargent 0:30

1426032 Begs, 333106140 residues

total number of hits satisfying chosen parameters: 1426032

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

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3:  /cgn2_6/pdatatc/1/pubpaa/US06_NEW_PUB_dep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

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2	75	100.0	37	14	US-10-060-107-5	Sequence 5, Appl1
3	75	100.0	37	15	US-10-721-838-5	Sequence 5, Appl1
4	75	100.0	37	16	US-10-344-709C-15	Sequence 15, Appl1
5	75	100.0	111	16	US-10-344-709C-7	Sequence 7, Appl1
6	48	64.0	439	9	US-09-815-242-5696	Sequence 7, Appl1
7	48	64.0	497	14	US-10-358-917-14	Sequence 5666, Ap
8	48	64.0	497	15	US-10-282-122A-439S5	Sequence 14, Appl1
9	47	62.7	443	16	US-10-767-701-443A5	Sequence 43955, A
10	47	62.7	861	15	US-10-282-122A-52284	Sequence 44345, A
11	46	61.3	31	17	US-10-399-442A-2	Sequence 52284, A
12	46	61.3	32	16	US-10-344-709C-1	Sequence 2, Appl1
13	46	61.3	35	13	US-10-205-150-1	Sequence 1, Appl1

ALIGNMENTS

14	46	61.3	36	14	US-10-269-177A-2	Sequence 2, Appl 1
15	46	61.3	36	14	US-10-470-DA8B-559	Sequence 599, Appl 1
16	46	61.3	39	14	US-10-060-102-1	Sequence 1, Appl 1
17	46	61.3	39	15	US-10-721-833-1	Sequence 1, Appl 1
18	46	61.3	133	16	US-10-344-709C-5	Sequence 5, Appl 1
19	46	61.3	1111	15	US-10-282-122A-58098	Sequence 58098, A
20	46	61.3	1112	16	US-10-398-186-22	Sequence 22, Appl 1
21	45	60.0	552	15	US-10-282-122A-73834	Sequence 73834, A
22	45	60.0	552	17	US-10-472-928-878	Sequence 878, App
23	44	58.7	81	15	US-10-424-559-274937	Sequence 274937, Sequence 11957,
24	44	58.7	90	16	US-10-437-963-111957	Sequence 67643, A
25	44	58.7	504	15	US-10-425-114-67643	Sequence 26915,
26	43	57.3	51	15	US-10-424-559-264915	Sequence 243585,
27	43	57.3	59	15	US-10-424-559-243585	Sequence 6, Appl 1
28	43	57.3	38	15	US-10-155-433-6	Sequence 54900, A
29	43	57.3	49	15	US-10-425-114-54900	Sequence 215078,
30	43	57.3	63	15	US-10-424-559-215078	Sequence 208110,
31	43	57.3	625	15	US-10-424-559-208110	Sequence 10, Appl 1
32	43	57.3	1639	14	US-10-087-466-10	Sequence 148381,
33	42	56.0	60	16	US-10-437-963-148381	Sequence 536, App
34	42	56.0	358	17	US-10-472-928-536	Sequence 250653,
35	41	54.7	67	15	US-10-424-559-250653	Sequence 181959,
36	41	54.7	108	15	US-10-424-559-181959	Sequence 264276,
37	41	54.7	129	15	US-10-424-559-264276	Sequence 228715,
38	41	54.7	136	15	US-10-424-559-228715	Sequence 34, Appl 1
39	41	54.7	155	15	US-10-335-603A-34	Sequence 60391, A
40	41	54.7	161	16	US-10-767-701-60391	Sequence 2, Appl 1
41	41	54.7	178	13	US-10-015-179-2	Sequence 2, Appl 1
42	41	54.7	178	15	US-10-188-840-2	Sequence 32, Appl 1
43	41	54.7	178	15	US-10-437-963A-32	Sequence 170068,
44	41	54.7	209	16	US-10-437-963A-170068	Sequence 1396, Ap
45	41	54.7	216	15	US-10-296-115-1396	

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RESULT 1
US-10-131-433-1
; Sequence 1, Application US/10131433
; Publication No. US20030054422A1
; GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Devices
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131,433
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Lapine
US-10-131-433-1

Query Match      100.0%; Score 75; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY      1 RKFRRNKKKEKLKKIG 15
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Db      7 RKFRRNKKKEKLKKIG 21

RESULT 2
US-10-060-102-5
; Sequence 5, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STABLETON, JACK

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 14.2458 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-24

Sequence: 1 RKRNRKXKXKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74643064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	75	100.0	171	3	US-09-322-911-4
5	51	68.0	16	1	US-08-313-681A-11
6	51	68.0	16	3	US-09-322-911-11
7	47	62.7	18	4	US-09-322-911-10
8	46	61.3	33	5	PCT-US95-12080-4
9	46	61.3	3421	4	US-09-452-638-53
10	45	60.0	429	4	US-09-583-110-4660
11	45	60.0	531	4	US-09-107-433-5016
12	45	60.0	726	4	US-09-252-991A-26767
13	43	57.3	693	4	US-09-489-039A-8763
14	42	56.0	408	4	US-09-248-796A-15721
15	42	56.0	415	4	US-09-489-039A-13974
16	41	54.7	452	4	US-09-889-738-21
17	41	54.7	476	4	US-09-543-681A-7117
18	40	53.3	18	4	US-09-525-269A-3
19	40	53.3	319	4	US-09-252-991A-30168
20	40	53.3	336	4	US-09-735-846-25
21	40	53.3	343	2	US-08-599-171A-28
22	40	53.3	343	2	US-08-546-590B-28
23	40	53.3	343	3	US-09-069-226-28
24	40	53.3	343	3	US-09-412-184-28
25	40	53.3	524	4	US-09-248-796A-18625
26	40	53.3	898	4	US-09-585-858-37
27	40	53.3	898	4	US-10-270-878-37

28	40	53.3	956	4	US-09-107-532A-5007	Sequence 5007, Ap
29	39	52.0	18	1	US-07-725-331-29	Sequence 29, Appl
30	39	52.0	18	5	PCT-US91-05047-29	Sequence 29, Appl
31	39	52.0	74	4	US-09-248-796A-25957	Sequence 25957, A
32	39	52.0	87	4	US-09-248-796A-24551	Sequence 24551, A
33	39	52.0	96	4	US-09-732-210-707	Sequence 707, App
34	39	52.0	154	4	US-09-248-796A-27970	Sequence 27970, A
35	39	52.0	166	4	US-09-270-767-51496	Sequence 36279, A
36	39	52.0	166	4	US-09-248-796A-14758	Sequence 51496, A
37	39	52.0	231	4	US-09-134-001C-4678	Sequence 14758, A
38	39	52.0	306	3	US-09-498-520A-44	Sequence 4678, Ap
39	39	52.0	395	3	US-09-134-001C-3723	Sequence 44, Appl
40	39	52.0	396	4	US-09-502-540-15124	Sequence 3723, Ap
41	39	52.0	672	3	US-09-040-843-4	Sequence 15124, A
42	39	52.0	672	3	US-09-621-855-4	Sequence 4, Appl
43	39	52.0	817	4	US-09-710-279-50	Sequence 4, Appl
44	39	52.0	817	4	US-09-710-279-1528	Sequence 50, Appl
45	39	52.0	817	4	US-09-710-279-1528	Sequence 1528, Ap

ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower,
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 52.5838 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-24

Perfect score: 1 RFRFKIKKKKIG 15

Sequence: 1 RFRFKIKKKKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : 1: Geneseq16Dec04:*

2: geneseq1980s:*\n3: geneseq1990s:*\n4: geneseq2000s:*\n5: geneseq2001s:*\n6: geneseq2002s:*\n7: geneseq2003as:*\n8: geneseq2003bs:*\n9: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	75	100.0	21	4	AAB70666
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6	75	100.0	22	4	AAB70668
7	75	100.0	24	6	AAB34416
8	75	100.0	24	8	ADK70763
9	75	100.0	24	8	ADK70764
10	75	100.0	26	6	AAB34418
11	75	100.0	26	6	AAB34417
12	75	100.0	26	6	AAB34419
13	75	100.0	26	6	AAB34421
14	75	100.0	26	6	AAB34420
15	75	100.0	26	6	ADK70762
16	75	100.0	29	2	AAB45671
17	75	100.0	29	3	AAB70903
18	75	100.0	32	3	AAB28486
19	75	100.0	32	8	ADK70761
20	75	100.0	37	4	AAB70665
21	75	100.0	37	5	ABBO7711
22	75	100.0	37	5	ABP53272
23	75	100.0	38	4	AAB51193
24	75	100.0	142	8	ADK70796
25	75	100.0	171	5	ABBO7703

26	69	92.0	20	8	ADK70765
27	51	68.0	16	2	AAB45673
28	51	68.0	16	3	AAB07905
29	48	64.0	15	4	AAB70672
30	48	64.0	17	4	AAB70673
31	48	64.0	439	4	AAB34200
32	48	64.0	497	6	ABU16031
33	48	64.0	497	6	ADN14544
34	48	64.0	500	6	ABM72616
35	47	62.7	18	2	AAV57472
36	47	62.7	18	5	ABG69896
37	47	62.7	881	6	ABU24360
38	46	61.3	31	5	AAO15559
39	46	61.3	32	5	ABO7697
40	46	61.3	33	2	AAB94449
41	46	61.3	35	8	ADR84033
42	46	61.3	36	4	AA664421
43	46	61.3	36	5	AAU09819
44	46	61.3	36	5	ABG31966
45	46	61.3	36	5	ABG31663

ALIGNMENTS

RESULT 1
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ID AAB70671 standard; peptide; 15 AA.
XX AAB70671;
AC 15-MAY-2001 (first entry)
DT 15-MAY-2001 (first entry)
XX Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:24.
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:24.
XX Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiolic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX Oryctolagus cuniculus.
OS WO200112668-A1.
PN 22-FEB-2001.
PD 22-FEB-2001.
PF 18-AUG-2000; 2000WO-US022781.
XX 18-AUG-1999; 99US-0149886P.
PR (TOWA) UNITV TOWA RES FOUND.
PA (REGC) UNITV CALIFORNIA.
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
DR WPI; 2001-234911/24.
XX New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX Claim 1, Page 103; 137pp; English.
XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiolic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors, and in gene therapy. (I) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 13.0223 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-23

Perfect score: 104

Sequence: 1 LRKFRNKIKKIKGKIQG 21

Scoring table: BIOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	65	62.5	173	2 S70521	cathelin-related p
3	60	57.7	324	2 T07982	probable choline-p
4	60	57.7	326	2 T07983	choline-phosphate
5	57	54.8	329	2 T07981	probable choline-p
6	57	54.8	331	2 T07980	probable choline-p
7	54	51.9	332	2 H84730	probable phospholi
8	50	48.1	354	2 B75003	hypothetical prote
9	50	48.1	519	2 T51496	hypothetical prote
10	50	48.1	663	2 D97047	hypothetical prote
11	50	48.1	1163	2 GNMVY8	DNA ligase (NAD de
12	50	48.1	3411	1 GNMVY	genome polypeptid
13	50	48.1	3411	1 GNMVY	genome polypeptid
14	49	47.1	142	2 E70356	hypothetical prote
15	49	47.1	259	2 G01485	synthaxin - human
16	49	47.1	288	2 G01615	neuron-specific an
17	49	47.1	298	2 A38144	neuron cell memb
18	49	47.1	829	2 T33744	hypothetical prote
19	48	46.2	117	1 H71166	hypothetical prote
20	48	46.2	117	2 E75065	hypothetical prote
21	48	46.2	152	2 C72227	conserved hypotet
22	48	46.2	288	2 J00136	synapocanalin I -
23	48	46.2	293	2 T04951	synthaxin 1B - rat
24	48	46.2	293	2 T04951	hypothetical prote
25	48	46.2	293	2 T04951	hypothetical prote
26	48	46.2	293	2 T04951	hypothetical prote
27	47.5	45.7	274	2 C69444	endopeptidase (imp
28	47	45.2	166	2 S41731	antibacterial prot
29	47	45.2	174	2 P84426	hypothetical prote

30	47	45.2	188	1 F64494	conserved hypotet
31	47	45.2	249	2 E75181	ribonuclease ph (r
32	47	45.2	507	2 C82901	conserved hypotet
33	47	45.2	573	2 D90202	methionyl-tRNA syn
34	47	45.2	1631	1 SAZOK1	major merozoite su
35	47	45.2	1639	2 S05603	probable major sur
36	47	45.2	1640	2 A24594	signal recognition
37	46.5	44.7	167	2 S25360	N-acetylornithine
38	46.5	44.7	376	2 G70301	polypeptide deform
39	46	44.2	169	2 A82373	hypothetical prote
40	46	44.2	362	2 T22204	iron-sulfur cluste
41	46	44.2	369	2 F82333	hypothetical prote
42	46	44.2	392	2 B85363	hypothetical prote
43	46	44.2	533	2 T06153	hypothetical prote
44	46	44.2	1156	2 B70356	chromosome assembl
45	46	44.2	1236	2 T18459	hypothetical prote

ALIGNMENTS

RESULT 1

J01171
18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: J01171, PS0226

R/Larrick, J.W.; Morgan, J.G.; Paling, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: J01171, M01D:91554246; PMID:1883348

A/Accession: J01171

A/Molecule type: mRNA

A/Residues: 1-171 <LRR>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'OTGOL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match Best Local Similarity 100.0%; Score 104; DB 2; Length 171; Pred. No. 2.3e-06; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRKFRNKIKKIKGKIQG 21
Db 140 LRKFRNKIKKIKGKIQG 160

RESULT 2

S70521
cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521

R/Popova, A.B.; Zinovjeva, M.V.; Vlaser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bel

FEBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521, M01D:96326596; PMID:8706928

A/Accession: S70521

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-references: UNIPROT:P51437; EMBL:X94353; NID:91177533; PIDN:CAA64078.1; PID:911

F/1-29/Domain: signal sequence #status predicted <SIG>

F/24-144/Domain: propeptide #status predicted <PRO>

F/145-173/Product: cathelin-related protein #status predicted <MAT>

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Run on: May 2, 2005, 13:03:56 ; Search time 57.1341 Seconds
(without 31 iterations)

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-23
Perfect score: 104
Sequence: 1 LKRFNRIKEKLKKIGQKIG 21

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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searched:      1426032 seqs, 333106140 residues
Total number of hits satisfying chosen parameters: 1426032

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubppa/PC7_NEW_PUB.dep:*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.dep:*
- 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.dep:*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.dep:*
- 6: /cgn2_6/ptodata/1/pubppa/PC7US_PUBCOMB.dep:*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.dep:*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.dep:*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.dep:*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.dep:*
- 11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.dep:*
- 12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.dep:*
- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.dep:*
- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.dep:*
- 15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.dep:*
- 16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.dep:*
- 17: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.dep:*
- 18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.dep:*
- 19: /cgn2_6/ptodata/1/pubppa/US10C_NEW_PUB.dep:*
- 20: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	104	100.0	32	14	US-10-131-433-1	Sequence 1, Appl
2	104	100.0	37	14	US-10-060-103-5	Sequence 5, Appl
3	104	100.0	37	15	US-10-721-838-5	Sequence 5, Appl
4	104	100.0	37	16	US-10-344-709C-15	Sequence 15, Appl
5	104	100.0	171	16	US-10-344-709C-7	Sequence 7, Appl
6	65	62.5	31	17	US-10-399-442A-2	Sequence 2, Appl
7	65	62.5	32	16	US-10-344-709C-1	Sequence 1, Appl
8	65	62.5	36	17	US-10-470-048B-599	Sequence 599, Appl
9	65	62.5	39	14	US-10-060-102-1	Sequence 1, Appl
10	65	62.5	39	15	US-10-721-839-1	Sequence 1, Appl
11	65	62.5	173	16	US-10-344-709C-5	Sequence 5, Appl
12	60	57.7	324	15	US-10-389-556C-1171	Sequence 1171, Appl
13	60	57.7	326	14	US-10-233-926-25	Sequence 25, Appl

ALIGNMENTS

14	60	55.7	326	15	US-10-389-566-1172	Sequence 1172, App
15	59	56.7	36	14	US-10-269-177A-2	Sequence 2, App11
16	58	55.8	129	15	US-10-424-599-264276	Sequence 264276, App
17	57	54.8	329	14	US-10-233-926-24	Sequence 24, App1
18	57	54.8	329	15	US-10-389-566-1173	Sequence 1173, App
19	57	54.8	331	14	US-10-233-926-23	Sequence 23, App1
20	57	54.8	331	15	US-10-389-566-1174	Sequence 1174, App
21	55	52.9	39	14	US-10-060-102-2	Sequence 2, App11
22	55	52.9	39	15	US-10-121-893-2	Sequence 2, App11
23	54	51.9	332	15	US-10-389-566-1816	Sequence 1816, App1
24	52	50.0	194	14	US-10-233-926-6	Sequence 6, App11
25	52	50.0	275	15	US-10-424-599-216383	Sequence 216383, App
26	52	50.0	318	15	US-10-389-566-673	Sequence 673, App
27	52	50.0	318	15	US-10-389-566-674	Sequence 674, App
28	52	50.0	363	14	US-10-233-926-20	Sequence 20, App1
29	52	50.0	1111	15	US-10-282-122A-58098	Sequence 58098, App
30	52	50.0	1112	16	US-10-398-186-22	Sequence 22, App1
31	51	49.0	35	13	US-10-205-150-1	Sequence 1, App11
32	50	48.1	60	16	US-10-437-965-148381	Sequence 148381, App
33	50	48.1	67	15	US-10-424-599-250653	Sequence 250653, App
34	50	48.1	63	15	US-10-282-122A-51673	Sequence 51673, App
35	49	47.1	51	15	US-10-424-599-264915	Sequence 264915, App
36	49	47.1	259	16	US-10-408-765A-807	Sequence 807, App
37	49	47.1	288	10	US-09-942-024-21	Sequence 21, App1
38	49	47.1	288	10	US-09-942-024-23	Sequence 23, App1
39	49	47.1	288	10	US-09-942-038-21	Sequence 21, App1
40	49	47.1	288	10	US-09-942-038-23	Sequence 23, App1
41	49	47.1	288	15	US-10-261-161-16	Sequence 16, App1
42	49	47.1	288	15	US-10-261-161-18	Sequence 18, App1
43	49	47.1	288	15	US-10-466-533-1	Sequence 1, App1
44	49	47.1	312	15	US-10-389-566-603	Sequence 603, App
45	49	47.1	443	16	US-10-767-701-44345	Sequence 44345, App

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RESULT 1
US-10-131-433-1
; Sequence 1, Application US/1011433
; Publication No. US20030054422A1
; GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131,433
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Lapine
; US-10-131-433-1

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Query Match          100.0%; Score 104; DB 14; Length 32;
Best Local Similarity 100.0%; Fred. No. 5e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy      1 LKRPNKIKETLKKIGQKIQG 21
        |||
Db      6 LKRPNKIKETLKKIGQKIQG 26

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 19.9441 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-23

Perfect score: 104

Sequence: 1 LRFRNKIKKKIKGKIOG 21

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	171	1	US-08-313-681A-4
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3	92	88.5	29	1	US-08-313-681A-7
4	92	88.5	29	3	US-09-322-911-7
5	65	62.5	33	5	PCT-US95-12080-4
6	60	57.7	326	4	US-09-735-846-25
7	57	54.8	329	4	US-09-735-846-24
8	57	54.8	331	4	US-09-735-846-23
9	55	52.9	16	1	US-08-313-681A-11
10	55	52.9	16	3	US-09-322-911-11
11	52	50.0	194	4	US-09-735-846-6
12	52	50.0	363	4	US-09-735-846-20
13	50	48.1	3421	4	US-09-452-638-53
14	49	47.1	259	4	US-08-393-985-25
15	49	47.1	259	4	US-09-509-738C-25
16	49	47.1	263	1	US-08-393-985-23
17	49	47.1	285	1	US-08-393-985-2
18	49	47.1	288	1	US-08-337-602-4
19	49	47.1	288	3	US-08-558-135-4
20	49	47.1	288	3	US-08-819-286-3
21	49	47.1	434	4	US-09-489-039A-8456
22	48	46.2	104	4	US-09-735-846-8
23	48	46.2	158	1	US-08-356-397-4
24	48	46.2	288	1	US-08-356-397-2
25	48	46.2	288	1	US-08-393-985-4
26	48	46.2	288	4	US-09-509-738C-26
27	48	46.2	672	3	US-09-040-843-4

28	48	46.2	672	3	US-09-621-855-4	Sequence 4, Appl
29	48	46.2	866	3	US-09-040-843-2	Sequence 2, Appl
30	48	46.2	866	3	US-09-621-855-2	Sequence 2, Appl
31	47	45.2	18	4	US-09-525-269A-10	Sequence 10, Appl
32	47	45.2	90	4	US-09-489-039A-11599	Sequence 11599, A
33	47	45.2	141	4	US-09-270-767-42264	Sequence 42264, A
34	47	45.2	306	3	US-09-134-001C-4678	Sequence 4678, Ap
35	47	45.2	502	4	US-09-328-352-6968	Sequence 6968, Ap
36	46.5	44.7	343	2	US-08-599-171A-28	Sequence 28, Appl
37	46.5	44.7	343	2	US-08-646-590B-28	Sequence 28, Appl
38	46.5	44.7	343	3	US-09-069-226-28	Sequence 28, Appl
39	46.5	44.7	343	3	US-09-412-184-28	Sequence 28, Appl
40	46	44.2	22	3	US-08-940-095-74	Sequence 28, Appl
41	46	44.2	22	3	US-08-940-095-93	Sequence 28, Appl
42	46	44.2	22	3	US-08-940-093-74	Sequence 28, Appl
43	46	44.2	22	3	US-08-940-093-93	Sequence 28, Appl
44	46	44.2	22	3	US-08-940-096-74	Sequence 28, Appl
45	46	44.2	22	3	US-08-940-096-93	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STEET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 104; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 LRFRNKIKKKIKGKIOG 21
140 LRFRNKIKKKIKGKIOG 160

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 73.6173 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-23

Perfect score: 104

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Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	104	100.0	21	4 AAB70670	AAB70670 Lupine RC
2	104	100.0	32	3 AAB28486	AAB28486 Rabbit 11
3	104	100.0	32	8 ADK70761	ADK70761 Rabbit CA
4	104	100.0	37	4 AAB70665	AAB70665 Lupine RC
5	104	100.0	37	5 ABB07711	ABB07711 Antimicro
6	104	100.0	37	5 ABP53272	ABP53272 Sheep nat
7	104	100.0	38	4 AAB51193	AAB51193 E. coli A
8	104	100.0	142	8 ADK70796	ADK70796 Rabbit CA
9	104	100.0	171	5 ABB07703	ABB07703 Rabbit pe
10	94	90.4	26	6 AAE34418	AAE34418 Rabbit CA
11	94	90.4	26	6 AAE34417	AAE34417 Rabbit CA
12	94	90.4	26	6 AAE34419	AAE34419 Rabbit CA
13	94	90.4	26	6 AAE34420	AAE34420 Rabbit CA
14	94	90.4	26	8 ADK70762	ADK70762 Rabbit CA
15	93	89.4	19	4 AAB70669	AAB70669 Lupine RC
16	93	89.4	22	4 AAB70668	AAB70668 Lupine RC
17	93	89.4	24	6 AAE34416	AAE34416 Rabbit RC
18	93	89.4	24	8 ADK70763	ADK70763 Rabbit CA
19	93	89.4	26	6 AAE34421	AAE34421 Rabbit CA
20	92	88.5	29	2 AAR45671	AAR45671 N terminu
21	92	88.5	29	3 AAB07903	AAB07903 Puerative
22	89	85.6	24	8 ADK70764	ADK70764 Rabbit CA
23	79	76.0	18	4 AAB70667	AAB70667 Lupine RC
24	79	76.0	21	4 AAB70666	AAB70666 Lupine RC
25	75	72.1	15	4 AAB70671	AAB70671 Lupine RC

26	73	70.2	15	4 AAB70672	AAB70672 Lupine RC
27	73	70.2	17	4 AAB70673	AAB70673 Lupine RC
28	73	70.2	20	8 ADK70765	ADK70765 Rabbit CA
29	65	62.5	31	5 AAO15559	AAO15559 Murine ca
30	65	62.5	32	5 ABB07697	ABB07697 Murine ca
31	65	62.5	33	2 AAR94449	AAR94449 Mouse nat
32	65	62.5	39	5 ABP53268	ABP53268 Mouse nat
33	65	62.5	173	5 ABB07701	ABB07701 Murine ca
34	60	57.7	324	8 ADA49167	ADA49167 O11-ABSC
35	60	57.7	326	6 ADA06238	ADA06238 Rape chol
36	60	57.7	326	8 ADA49168	ADA49168 O11-ABSC
37	60	57.7	326	8 AD017009	AD017009 Brasica
38	59	56.7	36	4 AAG66421	AAG66421 Mouse cat
39	59	56.7	36	5 AAU09819	AAU09819 Mouse cat
40	59	56.7	36	5 ABG31966	ABG31966 Mouse cat
41	59	56.7	36	5 ABG31663	ABG31663 Mouse cat
42	59	56.7	36	5 AAU76940	AAU76940 Mouse cat
43	59	56.7	36	6 ABP58358	ABP58358 Mouse cat
44	59	56.7	36	8 ADJ51139	ADJ51139 Murine ca
45	57	54.8	329	6 ADA06237	ADA06237 Rape chol

ALIGNMENTS

RESULT 1
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AC AAB70670;
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:23.
XX
XX Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
XX bactericidal; antibiotic; antiviral; microbial growth inhibitor;
XX proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryzococcus cuniculus.
XX
XX WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PR (IOWA) UNIV IOWA RES FOUND.
XX (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
XX Claim 1; Page 103; 137pp; English.
XX
XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SWAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (II) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 59.2821 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-22

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Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_03:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	171	1	CP18 RABIT
2	64	68.8	173	1	CRAN_MOUSE
3	61	65.6	511	2	Q7P8L9
4	57	61.3	171	2	Q71KM5
5	55	59.1	324	2	Q42621
6	55	59.1	326	2	Q42622
7	54	58.1	508	1	YU13 FUSNN
8	53	57.0	170	2	Q9GLV5
9	53	57.0	3787	2	Q811Z6
10	52	55.9	329	2	Q42620
11	52	55.9	331	2	Q42619
12	52	55.9	362	2	Q9BPM9
13	52	55.9	1111	1	YJEP HAEIN
14	50	53.8	224	2	Q6W9J9
15	50	53.8	235	2	Q6W9J1
16	50	53.8	239	2	Q7P6A4
17	50	53.8	668	2	Q891I0
18	50	53.8	811	1	COAT GMDNV
19	50	53.8	1901	2	Q86L69
20	49.5	53.2	420	2	Q86L69
21	49	52.7	133	2	Q86L69
22	49	52.7	142	2	Q66881
23	49	52.7	332	2	Q42555
24	49	52.7	332	2	Q92V56
25	49	52.7	400	2	Q89295
26	49	52.7	400	2	Q89297
27	49	52.7	400	2	Q89299
28	49	52.7	400	2	Q89304
29	49	52.7	400	2	Q89311
30	49	52.7	400	2	Q89315
31	49	52.7	400	2	Q89317

32	49	52.7	425	2	P96200	P96200 bacteroides
33	49	52.7	598	2	Q48537	Q48537 lactobacill
34	49	52.7	778	2	P89915	P89915 yellow feve
35	49	52.7	778	2	Q77X62	Q77X62 yellow feve
36	49	52.7	778	2	Q77X64	Q77X64 yellow feve
37	49	52.7	778	2	Q9W9B8	Q9W9B8 yellow feve
38	49	52.7	1163	1	POLG_YEPV8	P29165 yellow feve
39	49	52.7	3411	1	POLG_YEPV1	P03314 Y genome feve
40	49	52.7	3411	1	POLG_YEPV2	P19901 Y genome po
41	49	52.7	3411	2	Q91857	Q91857 yellow feve
42	49	52.7	3411	2	Q98803	Q98803 yellow feve
43	49	52.7	3411	2	Q6DV88	Q6DV88 yellow feve
44	49	52.7	3411	2	Q6J3P1	Q6J3P1 yellow feve
45	49	52.7	3411	2	Q6PX46	Q6PX46 yellow feve

ALIGNMENTS

RESULT 1
CP18 RABIT
ID CP18 RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Anticicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP TISSUE=bone marrow;
RC MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN [3]
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.W., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8133956; DOI=10.1016/0014-5793(94)80395-1;
RA Tosai A., Scocchi M., Skerlavaj B., Genaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using sw model.

Run on: May 2, 2005, 12:21:40 ; Search time 11.7821 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-22

Perfect score: 93
Sequence: 1 LRKFRNKIKELKKIGOKI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	171	2 JQ1171	18K lipopolysaccha
2	64	68.8	173	2 S70521	cathelin-related p
3	55	59.1	324	2 T07982	probable choline-P
4	55	59.1	326	2 T07983	choline-phosphate
5	52	55.9	329	2 T07981	probable choline-P
6	52	55.9	331	2 T07980	probable choline-P
7	49	52.7	142	2 E70356	hypothetical prote
8	49	52.7	332	2 H84730	hypothetical prote
9	49	52.7	1163	1 GNMVY8	genome polyprotein
10	49	52.7	3411	1 GNMVY	genome polyprotein
11	49	52.7	3411	1 GNMVY	genome polyprotein
12	48	51.6	152	2 C72227	conserved hypotet
13	48	51.6	293	2 T04851	hypothetical prote
14	48	51.6	497	2 E90661	hypothetical prote
15	47.5	51.1	274	2 C69444	conserved hypotet
16	47	50.5	174	2 F84426	hypothetical prote
17	47	50.5	259	2 G01485	synthaxin - human
18	47	50.5	288	2 J01615	neuron-specific an
19	47	50.5	298	2 A38141	neutonal cell memb
20	47	50.5	507	2 C82501	conserved hypotet
21	46	49.5	166	2 S41731	antibacterial prot
22	46	49.5	169	2 A82373	polypeptide deform
23	46	49.5	288	2 J00136	synaptocanalin I -
24	46	49.5	362	2 B48213	synaxin 18 - rat
25	46	49.5	362	2 T22204	hypothetical prote
26	46	49.5	519	2 T51496	hypothetical prote
27	46	49.5	1236	2 T18459	hypothetical prote
28	45	48.4	189	2 C64469	hypothetical prote
29	45	48.4	443	2 A82872	ATP-dependent RNA

30	45	48.4	486	2 S74319	RTG3 protein - yea
31	45	48.4	522	2 A95059	hypothetical prote
32	45	48.4	522	2 H97927	type I site-specif
33	45	48.4	573	2 D90202	methionyl-tRNA syn
34	45	48.4	663	2 D97047	DNA ligase (NAD de
35	45	48.4	1631	1 SAZOK1	major merozoite su
36	45	48.4	1639	2 S05603	probable major sur
37	45	48.4	1640	2 A24594	conserved hypotet
38	44.5	47.8	121	2 H70471	hypothetical prote
39	44.5	47.8	399	2 D86322	hypothetical prote
40	44	47.3	109	2 G64379	hypothetical prote
41	44	47.3	119	2 C90351	hypothetical prote
42	44	47.3	175	2 A64330	hypothetical prote
43	44	47.3	178	2 H97293	hypoxanthine-guanl
44	44	47.3	188	2 E71157	probable CDP-alcoh
45	44	47.3	241	2 G86355	hypothetical prote

ALIGNMENTS

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: JQ1171, PS0226

R/Larrick, J.W.; Morgan, J.G.; Pallings, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171, MUID:91354246; PMID:1883348

A/Accession: JQ1171

A/Molecule type: mRNA

A/Residues: 1171 <LAR>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'OIGOLL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match Best Local Similarity 100.0%; Score 93; DB 2; Length 171;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRKFRNKIKELKKIGOKI 19
Db 140 LRKFRNKIKELKKIGOKI 158

RESULT 2

S70521

cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521

R/Popuueva, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bel

FEBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521, MUID:96326596; PMID:8706928

A/Accession: S70521

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-references: UNIPROT:P51437; EMBL:X94353; NID:G1177533; PTDN:CAA64078.1; PTD:911

C/Superfamily: cathelin; cystatin homology

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-144/Domain: propeptide #status predicted <PRO>

F/145-173/Product: cathelin-related protein #status predicted <MAT>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 18.0447 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744d-22

Perfect score: 93

Sequence: 1 LRFRNKIKKIKIGOKI 19

Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	171	1	US-08-313-681A-4
2	93	100.0	171	3	US-09-322-911-4
3	87	93.5	29	1	US-08-313-681A-7
4	87	93.5	29	3	US-09-322-911-7
5	64	68.8	33	5	PCT-US95-12080-4
6	55	59.1	16	1	US-08-313-681A-11
7	55	59.1	16	3	US-09-322-911-11
8	55	59.1	326	4	US-09-735-846-25
9	52	55.9	329	4	US-09-735-846-25
10	52	55.9	331	4	US-09-735-846-24
11	49	52.7	3421	4	US-09-452-638-53
12	47	50.5	18	4	US-09-525-269A-10
13	47	50.5	190	4	US-08-393-985-25
14	47	50.5	194	4	US-09-735-846-6
15	47	50.5	259	4	US-09-509-738C-25
16	47	50.5	263	1	US-08-393-985-23
17	47	50.5	283	1	US-08-393-985-2
18	47	50.5	288	1	US-08-337-602-4
19	47	50.5	288	3	US-08-558-135-4
20	47	50.5	306	3	US-08-819-286-3
21	47	50.5	363	4	US-09-134-001C-4678
22	46	49.5	27	1	US-09-735-846-20
23	46	49.5	27	1	US-08-231-730A-15
24	46	49.5	27	1	US-08-427-001C-15
25	46	49.5	27	1	US-08-457-798-15
26	46	49.5	27	1	US-08-457-171-15
27	46	49.5	27	2	US-08-505-486-15

28	46	49.5	27	2	US-08-505-486-62	Sequence 62, Appl
29	46	49.5	27	3	US-08-689-489C-15	Sequence 15, Appl
30	46	49.5	27	3	US-08-801-028-15	Sequence 15, Appl
31	46	49.5	27	3	US-08-801-028-62	Sequence 62, Appl
32	46	49.5	27	3	US-09-340-154-15	Sequence 15, Appl
33	46	49.5	27	3	US-09-340-154-62	Sequence 62, Appl
34	46	49.5	27	3	US-09-232-802A-15	Sequence 15, Appl
35	46	49.5	27	4	US-09-482-611B-15	Sequence 15, Appl
36	46	49.5	27	4	US-09-482-611B-62	Sequence 62, Appl
37	46	49.5	27	5	US-09-019-922A-15	Sequence 15, Appl
38	46	49.5	27	5	PCT-US94-06176-15	Sequence 15, Appl
39	46	49.5	27	5	PCT-US95-04335-15	Sequence 15, Appl
40	46	49.5	27	5	PCT-US95-04718-15	Sequence 15, Appl
41	46	49.5	27	5	PCT-US95-09338-15	Sequence 15, Appl
42	46	49.5	27	5	PCT-US95-09338-62	Sequence 62, Appl
43	46	49.5	27	5	PCT-US95-09339-15	Sequence 15, Appl
44	46	49.5	27	5	PCT-US95-09339-62	Sequence 62, Appl
45	46	49.5	27	5	PCT-US95-09339-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishima
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 93; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 LRFRNKIKKIKIGOKI 19
DB 140 LRFRNKIKKIKIGOKI 158

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 66.6061 Seconds

(without alignment)
110.327 Million cell updates/sec

Title: US-09-642-744D-22

Perfect score: 93
Sequence: 1 LRRFRNKKIKKKIKGKI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	19	4 AAB70669	Aab70669 Lupine RC
2	93	100.0	21	4 AAB70670	Aab70670 Lupine RC
3	93	100.0	22	4 AAB70668	Aab70668 Lupine RC
4	93	100.0	24	6 AAE34416	Aae34416 Rabbit RC
5	93	100.0	24	8 ADK70763	Adk70763 Rabbit CA
6	93	100.0	26	6 AAE34418	Aae34418 Rabbit CA
7	93	100.0	26	6 AAE34417	Aae34417 Rabbit CA
8	93	100.0	26	6 AAE34419	Aae34419 Rabbit CA
9	93	100.0	26	6 AAE34421	Aae34421 Rabbit CA
10	93	100.0	26	6 AAE34420	Aae34420 Rabbit CA
11	93	100.0	32	8 ADK70762	Adk70762 Rabbit CA
12	93	100.0	32	3 AAB28486	Aab28486 Rabbit II
13	93	100.0	32	8 ADK70761	Adk70761 Rabbit CA
14	93	100.0	37	4 AAB70665	Aab70665 Lupine RC
15	93	100.0	37	5 AAB70711	Abb07711 Antimicro
16	93	100.0	37	5 AAB51272	Abp51272 Sheep nat
17	93	100.0	38	4 AAB51193	Aab51193 E. coli A
18	93	100.0	142	8 ABB07796	Abb07796 Rabbit CA
19	93	100.0	171	5 ABB07703	Abb07703 Rabbit PE
20	89	95.7	24	8 ADK70764	Adk70764 Rabbit CA
21	87	93.5	29	3 AAB45671	Aa45671 N terminu
22	87	93.5	29	3 AAB07903	Aab07903 Putative
23	79	84.9	18	4 AAB70667	Aab70667 Lupine RC
24	79	84.9	21	4 AAB70666	Aab70666 Lupine RC
25	75	80.6	15	4 AAB70671	Aab70671 Lupine RC

26	73	78.5	20	8 ADK70765	Adk70765 Rabbit CA
27	64	68.8	31	5 AAO15559	Aao15559 Murine ca
28	64	68.8	32	5 ABB07697	Abb07697 Murine ca
29	64	68.8	33	2 AAB94449	Aab94449 Mouse ant
30	64	68.8	39	5 ABP53268	Abp53268 Mouse nat
31	64	68.8	173	5 ABB07701	Abb07701 Murine ca
32	62	66.7	15	4 AAB70672	Aab70672 Lupine RC
33	62	66.7	17	4 AAB70673	Aab70673 Lupine RC
34	58	62.4	36	4 AAG66421	Aag66421 Mouse cat
35	58	62.4	36	5 AAU09819	Aau09819 Mouse cat
36	58	62.4	36	5 ABG31966	Abg31966 Mouse cat
37	58	62.4	36	5 AAG31663	Aag31663 Mouse cat
38	58	62.4	36	5 AAU76940	Aau76940 Mouse cat
39	58	62.4	36	6 ABP58358	Abp58358 Mouse cat
40	58	62.4	36	8 ADJ51139	Adj51139 Murine ca
41	55	59.1	16	2 AAR45673	Aar45673 RMP hepa
42	55	59.1	16	3 AAB07905	Aab07905 Heparin-B
43	55	59.1	324	8 ADJ49167	Adj49167 O11-aseoc
44	55	59.1	326	6 ADA06238	Ada06238 Rape chol
45	55	59.1	326	8 ADJ49168	Adj49168 O11-aseoc

ALIGNMENTS

RESULT 1
AAB70669
ID AAB70669 standard; peptide; 19 AA.
XX
AC AAB70669;
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:22.
XX
KW Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryzocolagus cuniculus.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX
DR WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (I) of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SMAP 29 cathelicidin family peptide, and AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (II) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
XX

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 68.6425 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-21
Perfect score: 108
Sequence: 1 RKRLRKFRANKIKKXIGQKI 22

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	171	1	CP18 RABIT
2	64	59.3	173	1	GRAM MOUSE
3	61	56.5	511	2	Q7P8I9
4	60	55.6	324	2	Q42621
5	60	55.6	326	2	Q42622
6	58	53.7	170	2	Q9GLV5
7	57	52.8	171	2	Q71KMS
8	57	52.8	329	2	Q42620
9	57	52.8	331	2	Q42619
10	54	50.0	331	2	Q42555
11	54	50.0	332	2	Q92V56
12	54	50.0	400	2	Q89295
13	54	50.0	400	2	Q89297
14	54	50.0	400	2	Q89299
15	54	50.0	400	2	Q89304
16	54	50.0	400	2	Q89311
17	54	50.0	400	2	Q89317
18	54	50.0	508	1	YJ13 FUSNN
19	54	50.0	778	2	P89915
20	54	50.0	778	2	Q77X62
21	54	50.0	778	2	Q77X64
22	54	50.0	778	2	Q9W9B8
23	54	50.0	3411	1	POLG-YEFV1
24	54	50.0	3411	1	POLG-YEFV2
25	54	50.0	3411	2	O91857
26	54	50.0	3411	2	O98803
27	54	50.0	3411	2	O6DV88
28	54	50.0	3411	2	O6U3P1
29	54	50.0	3411	2	O6PX46
30	54	50.0	3411	2	O89275
31	54	50.0	3411	2	O89276

ALIGNMENTS

RESULT 1	CP18 RABIT	STANDARD	PRT	171 AA.
AC	P25230			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).			
GN	Name=CAP18;			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_Taxid=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=91354246; PubMed=1883348;			
RA	Larick J.W., Morgan J.G., Palling I., Hirata M., Yen M.H.;			
RT	"Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";			
RL	Biochem. Biophys. Res. Commun. 179:170-175(1991).			
RN	[2]			
RP	SEQUENCE OF 135-159, AND CHARACTERIZATION.			
RX	MEDLINE=94178952; PubMed=812348;			
RA	Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palling I.,			
RA	Wilson D., Yen M.H., Wright S.C., Larick J.W.;			
RT	"Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";			
RL	Infect. Immun. 62:1421-1426(1994).			
RN	[3]			
RP	SEQUENCE OF 135-154, AND CHARACTERIZATION.			
RX	MEDLINE=94075827; PubMed=8254193;			
RA	Larick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,			
RA	Cavallion J.-M., Warren H.S., Wright S.C.;			
RT	"A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";			
RL	J. Immunol. 152:231-240(1994).			
RN	[4]			
RP	CHARACTERIZATION.			
RA	MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;			
RA	Tosai A., Scocchi M., Sherlavaj B., Gennaro R.;			
RT	"Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";			
RL	FEBS Lett. 339:108-112(1994).			
RN	[5]			
RP	STRUCTURE BY NMR OF 135-166.			
RX	MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;			
RA	Chen C., Brock R., Luh F., Chou P.-J., Larick J.W., Huang R.-F.,			
RA	Huang T.-H.;			
RT	"The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";			
RL	FEBS Lett. 370:46-52(1995).			

32	54	50.0	3411	2	O89277	O89277 yellow feve
33	54	50.0	3411	2	O89278	O89278 yellow feve
34	54	50.0	3411	2	O9YRV3	O9YRV3 yellow feve
35	54	50.0	3411	2	O9YVNO	O9YVNO yellow feve
36	54	50.0	3411	2	O9YVNI	O9YVNI yellow feve
37	54	50.0	3411	2	O9YVNI	O9YVNI yellow feve
38	53	49.1	178	2	O60831	O60831 homo sapien
39	53	49.1	178	2	O9JIG8	O9JIG8 m dxiim39e
40	53	49.1	400	2	O89315	O89315 yellow feve
41	53	49.1	809	2	O6FTT3	O6FTT3 candida gla
42	53	49.1	1163	1	POLG-YEFV8	P29165 yellow feve
43	53	49.1	3787	2	O81126	O81126 plasmodium
44	52	48.1	123	2	O9NHL6	O9n16 plasmodium
45	52	48.1	228	2	O74MC7	O74mc7 nanosarchaeu

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:21:40 / Search time 13.6425 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-21

Perfect score: 108

Sequence: 1 RKRLKFRNKIKKKIKGKI 22

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	171	2 JQ1171	18K lipopolysaccharide-binding protein precursor - rabbit
2	64	59.3	173	2 S70521	cathelin-related protein - mouse
3	60	55.6	324	2 T07982	probable choline-P
4	60	55.6	326	2 T07983	cholesterol-phosphate
5	57	52.8	329	2 T07981	probable choline-P
6	57	52.8	331	2 T07980	probable phospholipid
7	54	50.0	332	2 H84730	probable phospholipid
8	54	50.0	3411	1 GNMVY	genome polypeptide
9	54	50.0	3411	1 GNMVY	genome polypeptide
10	53	49.1	1163	1 GNMVY	genome polypeptide
11	51	47.2	166	2 S41731	genome polypeptide
12	51	47.2	241	2 G86355	antibacterial protein
13	50	46.3	73	2 T03182	hypothetical protein
14	50	46.3	831	2 S44843	hypothetical protein
15	49.5	45.8	121	2 H70471	hypothetical protein
16	49.5	45.8	121	2 S44843	hypothetical protein
17	49	45.4	142	2 T50459	DNA repair and recombination
18	49	45.4	354	2 B70356	hypothetical protein
19	48.5	44.9	312	2 H81339	hypothetical protein
20	48.5	44.9	477	2 A75052	cysteine-rich protein
21	48	44.4	96	2 F72228	conserved hypothetical protein
22	48	44.4	152	2 C72227	hypothetical protein
23	48	44.4	293	2 T04951	hypothetical protein
24	48	44.4	497	2 E90601	hypothetical protein
25	48	44.4	507	2 C82901	conserved hypothetical protein
26	48	44.4	1233	2 I54383	conserved hypothetical protein
27	47.5	44.0	274	2 C69444	conserved hypothetical protein
28	47.5	44.0	274	2 D70410	cysteine-rich protein
29	47.5	44.0	976	2 A97104	Zn-dependent metal

30	47	43.5	94	2 T43076	hypothetical protein
31	47	43.5	153	2 JN0344	myoglobin - Balkan
32	47	43.5	167	2 S68967	antibacterial peptide
33	47	43.5	174	2 F84426	hypothetical protein
34	47	43.5	259	2 S57283	14-3-3 brain protein
35	47	43.5	259	2 G01485	synaptobrevin - human
36	47	43.5	288	2 JN0466	epimorphin - human
37	47	43.5	288	2 JQ1615	neuron-specific antigen
38	47	43.5	298	2 A38141	neuron-specific antigen
39	47	43.5	305	2 T23929	neuron-specific antigen
40	47	43.5	655	2 S57119	hypothetical protein
41	47	43.5	655	2 T50203	hypothetical protein
42	47	43.5	788	2 E97188	yeast RNase P/MP
43	47	43.5	822	2 S77112	DNA mismatch repair
44	46	42.6	162	2 H70314	hypothetical protein
45	46	42.6	169	2 A82373	polypeptide domain

ALIGNMENTS

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: JQ1171; P80226

R/Larrick, J.W.; Morgan, J.G.; Palling, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171; MUID:91354246; PMID:1883348

A/Accession: JQ1171

A/Molecule type: mRNA

A/Residues: 1-171 <LA>

A/Experimental source: bone marrow

A/Accession: P80226

A/Molecule type: protein

A/Residues: 135-159, 'QIGQL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 108; DB 2; Length 171;

Best Local Similarity 100.0%; Pred. No. 2.6e-06;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRLKFRNKIKKKIKGKI 22

DB 137 RKRLKFRNKIKKKIKGKI 158

RESULT 2

S70521

cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521

R/Popova, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.B.; Bel

EBBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521; MUID:96326596; PMID:8706928

A/Accession: S70521

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-reference: UNIPROT:P51437; EMBL:X94353; NID:G1177533; PIDN:CAA64078.1; PID:911

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-144/Domain: propeptide #status predicted <PRO>

F/145-173/Product: cathelin-related protein #status predicted <MAT>

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OM protein - protein search, using ew model

Run on: May 2, 2005, 13:03:56 ; Search time 59.8548 Seconds

(without alignment)
122.435 Million cell updates/sec

Title: US-09-642-744D-21

Sequence: 1 RKRLRRFKRKIKKIKGOKI 22

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubppa/PTC_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubppa/PTCUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	32	14	US-10-131-433-1
2	108	100.0	37	14	US-10-060-102-5
3	108	100.0	37	15	US-10-721-839-5
4	108	100.0	37	16	US-10-344-709C-15
5	108	100.0	171	16	US-10-344-709C-7
6	64	59.3	31	17	US-10-399-442A-2
7	64	59.3	32	16	US-10-344-709C-1
8	64	59.3	36	17	US-10-470-048B-599
9	64	59.3	39	14	US-10-060-102-1
10	64	59.3	39	15	US-10-721-839-1
11	64	59.3	173	16	US-10-344-709C-5
12	60	55.6	324	15	US-10-389-566-1171
13	60	55.6	326	14	US-10-233-926-25

14	60	55.6	326	15	US-10-389-566-1172	Sequence 1172, Ap
15	58	53.7	36	14	US-10-269-171A-2	Sequence 2, Appl1
16	57	52.8	329	14	US-10-233-926-24	Sequence 24, Appl1
17	57	52.8	329	15	US-10-389-566-1173	Sequence 1173, Ap
18	57	52.8	331	15	US-10-233-926-23	Sequence 23, Appl
19	57	52.8	331	15	US-10-389-566-1174	Sequence 1174, Ap
20	56	51.9	51	15	US-10-424-599-264915	Sequence 264915,
21	54	50.0	39	14	US-10-060-102-2	Sequence 2, Appl1
22	54	50.0	39	15	US-10-721-839-2	Sequence 2, Appl1
23	54	50.0	194	14	US-10-233-926-6	Sequence 6, Appl1
24	54	50.0	318	15	US-10-389-566-673	Sequence 673, App
25	54	50.0	332	15	US-10-389-566-674	Sequence 674, App
26	54	50.0	332	15	US-10-389-566-1816	Sequence 1816, Ap
27	54	50.0	363	14	US-10-233-926-20	Sequence 20, Appl
28	53	49.1	155	15	US-10-336-603A-34	Sequence 34, Appl
29	53	49.1	178	13	US-10-015-179-2	Sequence 2, Appl1
30	53	49.1	178	15	US-10-188-840-2	Sequence 2, Appl1
31	53	49.1	178	15	US-10-336-603A-32	Sequence 32, Appl1
32	53	49.1	641	16	US-10-437-963-181519	Sequence 181519,
33	52	48.1	1111	15	US-10-282-122A-58098	Sequence 58098, A
34	52	48.1	1112	16	US-10-398-186-22	Sequence 181519,
35	51	47.2	23	10	US-09-820-053A-55	Sequence 22, Appl
36	51	47.2	23	14	US-10-109-171-55	Sequence 55, Appl
37	51	47.2	35	13	US-10-205-150-1	Sequence 55, Appl
38	50	46.3	59	15	US-10-424-599-243585	Sequence 243585,
39	50	46.3	67	15	US-10-424-599-250653	Sequence 250653,
40	50	46.3	83	16	US-10-437-963-148201	Sequence 148201,
41	50	46.3	257	16	US-10-437-963-116556	Sequence 116556,
42	50	46.3	258	9	US-09-828-447-13	Sequence 13, Appl
43	50	46.3	116	14	US-10-032-585-7782	Sequence 7782, Ap
44	49.5	45.8	112	16	US-10-767-701-35738	Sequence 35738, A
45	49.5	45.4	123	9	US-09-820-893-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-10-131-433-1
Sequence 1, Application US/10131433
Publication No. US20030054422A1
GENERAL INFORMATION:
APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolysaccharide Immunoassay
CURRENT APPLICATION NUMBER: US/10/131,433
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/09/545,180
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 32
TYPE: PRT
ORGANISM: Lactine
US-10-131-433-1

Query Match 100.0%; Score 108; DB 14;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRLRRFKRKIKKIKGOKI 22
|||||
Db 3 RKRLRRFKRKIKKIKGOKI 24

RESULT 2
US-10-060-102-5
Sequence 5, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 20.8939 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-21

Sequence: 1 RKRLKFRNKIKKXIGOKI 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A COMB pep.*
2: /cgn2_6/prodata/1/aa/5B COMB pep.*
3: /cgn2_6/prodata/1/aa/6A COMB pep.*
4: /cgn2_6/prodata/1/aa/6B COMB pep.*
5: /cgn2_6/prodata/1/aa/PCUS COMB pep.*
6: /cgn2_6/prodata/1/aa/backfilest1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	171	1	US-08-313-681A-4
2	108	100.0	171	3	US-09-322-911-4
3	102	94.4	29	3	US-08-313-681A-7
4	102	94.4	29	3	US-09-322-911-7
5	70	64.8	16	1	US-08-313-681A-11
6	70	64.8	16	1	US-09-322-911-11
7	64	59.3	33	5	PCT-US95-12080-4
8	60	55.6	326	4	US-09-735-846-25
9	57	52.8	329	4	US-09-735-846-24
10	54	50.0	331	4	US-09-735-846-23
11	54	50.0	194	4	US-09-735-846-6
12	54	50.0	363	4	US-09-735-846-20
13	54	50.0	3421	4	US-09-452-638-53
14	53	49.1	37	1	US-08-313-681A-6
15	53	49.1	37	3	US-09-322-911-6
16	50	46.3	258	4	US-09-828-447-13
17	50	46.3	486	4	US-09-248-796A-18727
18	49	45.4	18	4	US-09-525-269A-10
19	49	45.4	123	4	US-09-148-545-187
20	49	45.4	123	4	US-09-148-545-243
21	49	45.4	188	4	US-09-695-795A-6
22	49	45.4	452	4	US-09-889-738-21
23	48	44.4	223	4	US-09-344-624-12
24	48	44.4	269	4	US-09-744-989C-3
25	48	44.4	287	4	US-09-744-989C-1
26	48	44.4	287	4	US-09-744-989C-5
27	48	44.4	1244	4	US-09-949-016-11702

28	47	43.5	103	3	US-09-308-388-1	Sequence 1, Appl
29	47	43.5	187	3	US-08-493-071-16	Sequence 16, Appl
30	47	43.5	190	1	US-08-393-985-25	Sequence 25, Appl
31	47	43.5	236	3	US-08-493-071-15	Sequence 15, Appl
32	47	43.5	259	4	US-09-509-738C-25	Sequence 25, Appl
33	47	43.5	263	1	US-08-393-985-23	Sequence 23, Appl
34	47	43.5	277	1	US-08-690-457-5	Sequence 5, Appl
35	47	43.5	277	2	US-08-628-187-5	Sequence 5, Appl
36	47	43.5	277	3	US-08-493-071-3	Sequence 3, Appl
37	47	43.5	285	1	US-08-393-985-2	Sequence 2, Appl
38	47	43.5	287	1	US-08-690-457-4	Sequence 4, Appl
39	47	43.5	287	2	US-08-628-187-4	Sequence 4, Appl
40	47	43.5	287	3	US-08-493-071-2	Sequence 2, Appl
41	47	43.5	288	1	US-08-337-602-4	Sequence 4, Appl
42	47	43.5	288	1	US-08-690-457-3	Sequence 3, Appl
43	47	43.5	288	2	US-08-628-187-3	Sequence 3, Appl
44	47	43.5	288	3	US-08-558-135-4	Sequence 4, Appl
45	47	43.5	288	3	US-08-493-071-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 108; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 RKRLKFRNKIKKXIGOKI 22
137 RKRLKFRNKIKKXIGOKI 158

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 56.162 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-20

Perfect score: 89

Sequence: 1 KRLRRFRNKKIKKIKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	171	1	CP18_RABIT
2	53	59.6	809	2	P25230 oryctolagus
3	51	57.3	241	2	O6FTT3
4	50	56.2	166	1	MP36_PIG
5	50	56.2	173	1	CRAM_MOUSE
6	50	56.2	178	2	O60831
7	50	56.2	178	2	O60831
8	49	55.1	142	2	O66881
9	49	55.1	241	1	143B_ARATH
10	49	55.1	324	2	O42621
11	49	55.1	326	2	O42622
12	49	55.1	352	2	O8GVE3
13	48	53.9	113	2	O7RA52
14	48	53.9	321	2	O7RAY0
15	48	53.9	364	2	O7RMJ3
16	48	53.9	381	2	O978N0
17	48	53.9	439	2	O53589
18	48	53.9	497	2	O8NU03
19	48	53.9	497	2	O99R73
20	48	53.9	497	2	O7A3D9
21	48	53.9	497	2	O6G6B0
22	48	53.9	497	2	O6G6B0
23	48	53.9	238	2	O48537
24	47.5	53.4	274	2	O28716
25	47	52.8	121	2	O67804
26	47	52.8	141	2	O9NH77
27	47	52.8	257	1	O91E33
28	47	52.8	259	1	1433_CHLRB
29	47	52.8	400	2	O89295
30	47	52.8	400	2	O89297
31	47	52.8	400	2	O89299

ALIGNMENTS

RESULT 1	CP18_RABIT	STANDARD	PRT	171 AA.
ID	CP18_RABIT	P25230		
AC	P25230			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DE	Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).			
GN	Name=CAP18;			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.			
RC	TISSUE=bone marrow;			
RX	MEDLINE=91354246; PubMed=1883348;			
RA	Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;			
RT	"Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein."			
RL	Biochem. Biophys. Res. Commun. 179:170-175(1991).			
RN	[2]			
RP	SEQUENCE OF 135-159, AND CHARACTERIZATION.			
RX	MEDLINE=94178952; PubMed=8132348;			
RA	Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I.,			
RT	Wilson D., Yen M.H., Wright S.C., Larrick J.W.;			
RL	"Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity."			
RN	Infect. Immun. 62:1421-1426(1994).			
RP	SEQUENCE OF 135-154, AND CHARACTERIZATION.			
RX	MEDLINE=94075827; PubMed=8254193;			
RA	Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,			
RT	Cavallion J.-M., Warren H.S., Wright S.C.;			
RL	"A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity."			
RN	J. Immunol. 152:231-240(1994).			
RP	[4]			
RX	CHARACTERIZATION.			
RA	MEDLINE=94148064; PubMed=8133956; DOI=10.1016/0014-5793(94)80395-1;			
RT	Tobai A., Scofield M., Skerlavaj B., Gennaro R.;			
RL	"Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes."			
RN	FEBS Lett. 339:108-112(1994).			
RP	[5]			
RX	STRUCTURE BY NMR OF 135-166.			
RA	MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;			
RT	Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F.,			
RL	Huang T.-H.;			
RT	"The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes."			
RL	FEBS Lett. 370:46-52(1995).			

32	47	52.8	400	2	O89304	O89304 yellow fever
33	47	52.8	400	2	O89311	O89311 yellow fever
34	47	52.8	400	2	O89315	O89315 yellow fever
35	47	52.8	400	2	O89317	O89317 yellow fever
36	47	52.8	511	2	O7P8U9	O7P8U9 fusobacteri
37	47	52.8	778	2	O7P8U9	O7P8U9 yellow fever
38	47	52.8	778	2	O77X62	O77X62 yellow fever
39	47	52.8	778	2	O77X64	O77X64 yellow fever
40	47	52.8	778	2	O9W9B8	O9W9B8 yellow fever
41	47	52.8	1163	1	POLG_YERF8	POLG_YERF8 yellow fever
42	47	52.8	1300	2	O7RB01	O7RB01 plasmodium
43	47	52.8	1321	2	O8IBV4	O8IBV4 plasmodium
44	47	52.8	1335	1	SOJO_XENTIA	SOJO_XENTIA plasmodium
45	47	52.8	3411	1	POLG_YERFV1	POLG_YERFV1 yellow fever
						P03314 Y genome po

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 11.162 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-20

Sequence: 1 KRLKRFNKKIKKKIKG 18

Scoring table: BIOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	171	2 J01171	18k lipopolysaccha
2	51	57.3	241	2 G86355	antibacterial prote
3	50	56.2	166	2 S41731	cathelin-related p
4	50	56.2	173	2 S70521	hypothetical prote
5	49	55.1	142	2 E70356	hypothetical prote
6	49	55.1	324	2 T07982	probable choline-p
7	49	55.1	326	2 T07983	choline-phosphate
8	48	53.9	497	2 B90061	hypothetical prote
9	47.5	53.4	274	2 C69444	conserved hypochet
10	47	52.8	121	2 H70471	conserved hypochet
11	47	52.8	259	2 S57283	14-3-3 brain prote
12	47	52.8	1163	1 GNMVY8	genome polypeptide
13	47	52.8	3411	1 GNMVY	genome polypeptide
14	47	52.8	3411	1 GNMVY	genome polypeptide
15	46	51.7	169	2 A82373	polypeptide deform
16	46	51.7	305	2 T23929	hypothetical prote
17	46	51.7	329	2 T07981	probable choline-p
18	46	51.7	331	2 T07980	probable choline-p
19	46	51.7	444	2 T24844	hypothetical prote
20	46	51.7	984	2 D70461	hypothetical prote
21	46	51.7	996	1 S42208	preprotein translo
22	45.5	51.1	661	2 T37753	NAD ADP-ribosyltra
23	45	50.6	153	2 JN0344	hypothetical prote
24	45	50.6	174	2 F84426	myoglobin - Baikal
25	45	50.6	463	2 B72500	hypothetical prote
26	45	50.6	522	2 A95059	probable seryl-trn
27	45	50.6	522	2 H97927	hypothetical prote
28	45	50.6	655	2 S57119	type 1 site-specific
29	45	50.6	831	2 S44843	hypothetical prote

30	45	50.6	1233	2 I54383	chromosome segrega
31	44.5	50.0	458	2 D70410	cytosolic axial fi
32	44	49.4	96	2 H69042	ribosomal protein
33	44	49.4	109	2 G64379	hypothetical prote
34	44	49.4	184	2 T04396	Richs protein - ba
35	44	49.4	254	2 H86355	probable 14-3-3 pr
36	44	49.4	288	2 UN0466	epimorphin - human
37	44	49.4	288	2 E85166	probable phosphoch
38	44	49.4	425	2 T24111	hypothetical prote
39	44	49.4	894	2 T15769	hypothetical prote
40	43.5	48.9	477	2 A75052	cysteiny1-cRNA syn
41	43.5	48.9	573	2 D90202	methionyl-cRNA syn
42	43.5	48.9	966	2 B84481	hypothetical prote
43	43	48.3	73	2 T03182	hypothetical prote
44	43	48.3	96	2 F72228	ribosomal protein
45	43	48.3	119	2 C90351	hypothetical prote

ALIGNMENTS

RESULT 1

J01171 18k lipopolysaccharide-binding protein precursor - rabbit

N:Alternate names: 18k cationic protein

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #ext_change 06-Dec-1996

C:Accession: J01171; PS0226

R:Larick, J.W.; Morgan, J.G.; Paling, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A:Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A:Reference number: J01171; PMID:91354246; PMID:1883348

A:Accession: J01171

A:Molecule type: mRNA

A:Residues: 1-171 <LA>

A:Experimental source: bone marrow

A:Accession: PS0226

A:Molecule type: protein

A:Residues: 135-159, 'QIGQL' <LA2>

A>Note: 157-Asp was also found

C:Superfamily: cathelin; cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-171/Product: 18k lipopolysaccharide-binding protein #status predicted <MAT>

Query Match Best Local Similarity 100.0%; Score 89; DB 2; Length 171;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLKRFNKKIKKKIKG 18

Db 138 KRLKRFNKKIKKKIKG 155

RESULT 2

G86355 hypothetical protein T16E15.9 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2001

C:Accession: G86355

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marshall

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A66141; MUID:21016719; PMID:11130712

A:Accession: G86355

A:Status: preliminary

A:Molecule type: DNA

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 48.9721 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-20

Sequence: 1 KRURKPRNKIKKIKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pcp:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pcp:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pcp:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pcp:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pcp:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pcp:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pcp:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pcp:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pcp:*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pcp:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pcp:*
12: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pcp:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pcp:*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pcp:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pcp:*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pcp:*
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18: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pcp:*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pcp:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	89	100.0	32	14	US-10-131-433-1
2	89	100.0	37	14	US-10-060-102-5
3	89	100.0	37	15	US-10-721-839-5
4	89	100.0	37	16	US-10-344-709C-15
5	89	100.0	171	16	US-10-344-709C-7
6	50	56.2	31	17	US-10-399-442A-2
7	50	56.2	32	16	US-10-344-709C-1
8	50	56.2	35	13	US-10-205-150-1
9	50	56.2	36	14	US-10-269-171A-2
10	50	56.2	36	17	US-10-470-048B-599
11	50	56.2	39	14	US-10-060-102-1
12	50	56.2	39	15	US-10-721-839-1
13	50	56.2	155	15	US-10-336-603A-34

14	50	56.2	173	16	US-10-344-709C-5	Sequence 5, Appl1
15	50	56.2	178	13	US-10-015-179-2	Sequence 2, Appl1
16	50	56.2	178	15	US-10-188-840-2	Sequence 2, Appl1
17	50	56.2	178	15	US-10-336-603A-32	Sequence 32, Appl1
18	50	56.2	258	9	US-09-828-447-13	Sequence 13, Appl1
19	49	55.1	324	15	US-10-389-566-1171	Sequence 1171, Ap
20	49	55.1	326	14	US-10-233-926-25	Sequence 25, Appl1
21	49	55.1	326	15	US-10-389-566-1172	Sequence 1172, Ap
22	48	53.9	51	15	US-10-424-559-264915	Sequence 264915, Sequence 243585,
23	48	53.9	51	15	US-10-424-559-264915	Sequence 5696, Ap
24	48	53.9	49	9	US-09-815-242-5696	Sequence 14, Appl1
25	48	53.9	497	14	US-10-358-917-14	Sequence 43955, A
26	48	53.9	497	15	US-10-282-122A-43955	Sequence 43945, A
27	47	52.8	443	16	US-10-767-701-44345	Sequence 52284, A
28	47	52.8	881	15	US-10-282-122A-52284	Sequence 81, Appl1
29	46	51.7	123	9	US-09-820-893-81	Sequence 92, Appl1
30	46	51.7	123	9	US-09-820-893-92	Sequence 187, App
31	46	51.7	123	9	US-09-818-876-187	Sequence 243, App
32	46	51.7	123	9	US-09-818-876-243	Sequence 187, App
33	46	51.7	123	10	US-09-148-545-187	Sequence 187, App
34	46	51.7	123	10	US-09-148-545-243	Sequence 187, App
35	46	51.7	123	15	US-10-607-565-81	Sequence 81, Appl1
36	46	51.7	123	15	US-10-607-565-92	Sequence 92, Appl1
37	46	51.7	169	14	US-10-197-666A-58	Sequence 58, Appl1
38	46	51.7	188	9	US-09-820-893-57	Sequence 57, Appl1
39	46	51.7	188	14	US-10-197-666A-54	Sequence 54, Appl1
40	46	51.7	188	15	US-10-607-565-57	Sequence 57, Appl1
41	46	51.7	224	15	US-10-424-559-156690	Sequence 156690, Sequence 24, Appl1
42	46	51.7	329	14	US-10-233-926-24	Sequence 1173, Ap
43	46	51.7	329	15	US-10-389-566-1173	Sequence 23, Appl1
44	46	51.7	331	14	US-10-233-926-23	Sequence 1174, Ap
45	46	51.7	331	15	US-10-389-566-1174	

ALIGNMENTS

RESULT 1
US-10-131-433-1
Sequence 1, Application US/10131433
Publication No. US20030054422A1
GENERAL INFORMATION:
APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolysaccharide Immunoassay
CURRENT APPLICATION NUMBER: US/10/131,433
CURRENT FILING DATE: 2002-04-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 32
TYPE: PRT
ORGANISM: Lactine
US-10-131-433-1

Query Match
Best Local Similarity 100.0%; Score 89; DB 14; Length 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRURKPRNKIKKIKIG 18
|||||
Db 4 KRURKPRNKIKKIKIG 21

RESULT 2
US-10-060-102-5
Sequence 5, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 17.095 Seconds

(without alignments)
78,601 Million cell updates/sec

Title: US-09-642-744d-20

Sequence: 1 KRLRRFKRKIKKKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	29	1 US-08-313-681A-7	Sequence 7, Appli
2	89	100.0	29	3 US-09-322-911-7	Sequence 7, Appli
3	89	100.0	171	1 US-08-313-681A-4	Sequence 4, Appli
4	89	100.0	171	3 US-09-322-911-4	Sequence 4, Appli
5	65	73.0	16	1 US-08-313-681A-11	Sequence 11, Appli
6	65	73.0	16	3 US-09-322-911-11	Sequence 11, Appli
7	50	56.2	33	5 PCT-US95-12080-4	Sequence 4, Appli
8	50	56.2	258	4 US-09-828-447-13	Sequence 10, Appli
9	49	55.1	18	4 US-09-525-269A-10	Sequence 13, Appli
10	49	55.1	326	4 US-09-735-846-25	Sequence 25, Appli
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12	47	52.8	3421	4 US-09-452-638-53	Sequence 51, Appli
13	46	51.7	18	1 US-09-725-331-29	Sequence 29, Appli
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15	46	51.7	123	4 US-09-148-545-187	Sequence 187, Appli
16	46	51.7	123	4 US-09-148-545-187	Sequence 243, Appli
17	46	51.7	188	4 US-09-695-795A-6	Sequence 6, Appli
18	46	51.7	329	4 US-09-735-846-24	Sequence 24, Appli
19	46	51.7	331	4 US-09-735-846-23	Sequence 23, Appli
20	45	50.6	223	4 US-09-344-624-12	Sequence 12, Appli
21	45	50.6	269	4 US-09-744-989C-3	Sequence 3, Appli
22	45	50.6	287	4 US-09-744-989C-1	Sequence 1, Appli
23	45	50.6	287	4 US-09-744-989C-5	Sequence 5, Appli
24	45	50.6	429	4 US-09-583-110-4660	Sequence 4660, Ap
25	45	50.6	531	4 US-09-107-433-5016	Sequence 5016, Ap
26	45	50.6	726	4 US-09-252-991A-26767	Sequence 26767, A
27	45	50.6	1244	4 US-09-949-016-11702	Sequence 11702, A

28	44	49.4	96	4 US-09-732-210-707	Sequence 707, App
29	44	49.4	103	3 US-09-308-388-1	Sequence 1, Appli
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32	44	49.4	277	1 US-08-690-457-5	Sequence 5, Appli
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36	44	49.4	287	2 US-08-628-187-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5616575
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Miehama
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

inhibiting the growth of drug-resistant microorganism strains in a host, and *Pseudomonas aeruginosa*, *Burkholderia cepacia* Alcalá et al. 1999.

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OM protein - protein search, using bw model

Run on: May 2, 2005, 13:03:56 ; Search time 57.1341 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-19

Perfect score: 104

Sequence: 1 GKRRLRKRFRNKIKKKKIG 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	104	100.0	37	16	US-10-344-709C-15
5	104	100.0	171	16	US-10-344-709C-7
6	53.5	51.4	112	16	US-10-767-701-35738
7	51.5	49.5	976	15	US-10-282-122A-51750
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10	51	49.0	641	16	US-10-437-963-181519
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14	50	48.1	36	14	US-10-269-171A-2	Sequence 2, Appl1
15	50	48.1	36	17	US-10-470-048B-599	Sequence 599, App
16	50	48.1	39	14	US-10-060-102-1	Sequence 1, Appl1
17	50	48.1	39	15	US-10-721-839-1	Sequence 1, Appl1
18	50	48.1	39	15	US-10-424-599-264915	Sequence 264915,
19	50	48.1	51	15	US-10-424-599-243585	Sequence 243585,
20	50	48.1	155	15	US-10-336-603A-34	Sequence 34, Appl1
21	50	48.1	173	16	US-10-344-709C-5	Sequence 3, Appl1
22	50	48.1	178	13	US-10-015-179-2	Sequence 2, Appl1
23	50	48.1	178	15	US-10-188-840-2	Sequence 32, Appl1
24	50	48.1	178	15	US-10-336-603A-32	Sequence 13, Appl1
25	50	48.1	258	9	US-09-828-447-13	Sequence 65, Appl1
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27	49.5	47.6	932	14	US-10-126-931A-65	Sequence 65, Appl1
28	49	47.1	324	15	US-10-389-566-1171	Sequence 1171, Ap
29	49	47.1	326	14	US-10-233-928-25	Sequence 25, Appl1
30	49	47.1	326	15	US-10-389-566-1172	Sequence 1172, Ap
31	49	47.1	336	15	US-10-424-599-184641	Sequence 184641,
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41	47	45.2	443	16	US-10-767-701-44345	Sequence 44345, A
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45	46	44.2	68	16	US-10-437-963-163080	Sequence 163080,

ALIGNMENTS

RESULT 1

US-10-131-433-1

Sequence 1, Application US/10131433

Publication No. US20030054422A1

GENERAL INFORMATION:

APPLICANT: UNILEVER, PLC

TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device

FILE REFERENCE: Lipopolysaccharide Immunoassay

CURRENT APPLICATION NUMBER: US/10/131,433

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US/09/545,180

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 32

TYPE: PRT

ORGANISM: Lاپine

US-10-131-433-1

Query Match

Best Local Similarity 100.0%; Score 104; DB 14; Length 32;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1 GKRRLRKRFRNKIKKKIG 21

RESULT 2

US-10-060-102-5

Sequence 5, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STABLETON, JACK

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 / Search time 19.9441 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744d-19

Sequence: 104
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Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	80	76.9	16	1 US-08-313-681A-11	Sequence 11, Appl
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7	53	51.0	3421	4 US-09-452-638-53	Sequence 53, Appl
8	50	48.1	33	5 PCT-US95-12080-4	Sequence 13, Appl
9	50	48.1	18	4 US-09-828-447-13	Sequence 10, Appl
10	49	47.1	37	4 US-09-525-269A-10	Sequence 6, Appl
11	49	47.1	37	1 US-08-313-681A-6	Sequence 6, Appl
12	49	47.1	37	3 US-09-322-911-6	Sequence 6, Appl
13	49	47.1	245	4 US-09-543-681A-6428	Sequence 6428, Ap
14	49	47.1	269	4 US-09-744-989C-3	Sequence 3, Appl
15	49	47.1	287	4 US-09-744-989C-1	Sequence 1, Appl
16	49	47.1	287	4 US-09-744-989C-5	Sequence 5, Appl
17	49	47.1	326	4 US-09-735-846-25	Sequence 25, Appl
18	49	47.1	452	4 US-09-889-738-21	Sequence 21, Appl
19	48	46.2	103	3 US-09-308-388-1	Sequence 15, Appl
20	48	46.2	236	3 US-08-493-071-15	Sequence 15, Appl
21	48	46.2	277	1 US-08-690-457-5	Sequence 5, Appl
22	48	46.2	277	2 US-08-628-187-5	Sequence 5, Appl
23	48	46.2	277	3 US-08-493-071-3	Sequence 4, Appl
24	48	46.2	287	1 US-08-690-457-4	Sequence 4, Appl
25	48	46.2	287	3 US-08-628-187-4	Sequence 4, Appl
26	48	46.2	287	3 US-08-493-071-2	Sequence 2, Appl
27	48	46.2	288	1 US-08-690-457-3	Sequence 3, Appl

ALIGNMENTS

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31	47	45.2	189	4 US-09-134-000C-4590	Sequence 4590, Ap
32	47	45.2	223	4 US-09-344-624-12	Sequence 12, Appl
33	47	45.2	1244	4 US-09-949-016-11702	Sequence 11702, A
34	46	44.2	18	1 US-07-725-331-29	Sequence 29, Appl
35	46	44.2	18	5 PCT-US91-05047-29	Sequence 29, Appl
36	46	44.2	123	4 US-09-148-545-187	Sequence 187, App
37	46	44.2	123	4 US-09-148-545-187	Sequence 243, App
38	46	44.2	188	4 US-09-695-795A-6	Sequence 6, Appl
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44	46	44.2	413	4 US-09-821-803A-7	
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RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishima
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET INFORMATION: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 73.6173 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-19

Perfect score: 104
Sequence: 1 GIRKRLRFRNKKIKLKKIG 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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17	104	100.0	42	8 ADK70796	Adk70796 Rabbit CA
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19	104	100.0	20	8 ADK70765	Adk70765 Rabbit pe
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21	98	94.2	22	4 AAB70667	Aab70667 Lupine RC
22	94	90.6	18	4 AAB70667	Aab70667 Lupine RC
23	89	85.6	16	2 AAB70667	Aab70667 RNP hepa
24	80	76.9	16	2 AAB70667	Aab70667 RNP hepa
25	80	76.9	16	3 AAB07905	Aab07905 Heparin-b

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33	51	49.0	334	5 ADG95663	Adg95663 Human nuc
34	51	49.0	334	6 ADA54882	Ada54882 Human pro
35	51	49.0	365	6 ABR41394	Ab41394 Human DIT
36	50	48.1	31	5 AAO15559	Aao15559 Murine ca
37	50	48.1	32	5 ABB07697	Abb07697 Murine ca
38	50	48.1	33	2 AAB94449	Aab94449 Mouse ant
39	50	48.1	35	8 ADR84033	Adr84033 Murine ca
40	50	48.1	36	5 AAG66421	Aag66421 Mouse cat
41	50	48.1	36	5 AAU09819	Aau09819 Mouse cat
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43	50	48.1	36	5 ABG31663	Abg31663 Mouse cat
44	50	48.1	36	5 AAU76940	Aau76940 Mouse cat
45	50	48.1	36	6 ABP58358	Abp58358 Mouse cat

ALIGNMENTS

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DT 15-MAY-2001 (first entry)
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XX
KW Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryctolagus cuniculus.
XX
PN NO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137p; English.
XX
CC AAB70668 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70668 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (II) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth of strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 37.4413 Seconds
(without alignments)

164.122 Million cell updates/sec

Title: US-09-642-744d-17

57

Sequence: 1 RRIKRIHITK 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_sprot.*
2: uniprot_tramb1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	73.7	500	1	TF3B_SCHPO
2	41	71.9	670	1	REP_BUCBP
3	40	70.2	414	2	094702
4	40	70.2	414	2	07XBY8
5	39	68.4	202	1	HAM1_AQUAB
6	39	68.4	210	2	092C15
7	39	68.4	4057	2	081YJ7
8	38	66.7	250	2	07M5F0
9	38	66.7	250	2	07WCY5
10	38	66.7	262	2	0720G5
11	38	66.7	272	2	08YFU6
12	38	66.7	475	2	075G18
13	38	66.7	574	1	SYP_BUCBP
14	38	66.7	598	2	07VTH0
15	38	66.7	623	1	Y014_MYCPN
16	38	66.7	638	2	08D796
17	38	66.7	660	2	07MEAO
18	38	66.7	878	2	07RY40
19	38	66.7	1157	2	07RON5
20	37	64.9	87	1	SSS1_SCYCA
21	37	64.9	125	2	09AVZ1
22	37	64.9	207	2	084604
23	37	64.9	295	2	013635
24	37	64.9	301	2	086FM8
25	37	64.9	302	2	081126
26	37	64.9	308	2	08R2C7
27	37	64.9	368	1	Y5FB_BACSU
28	37	64.9	415	2	09SPU4
29	37	64.9	428	2	08RTX5
30	37	64.9	467	2	06T1X3
31	37	64.9	491	2	09H8X2

32	37	64.9	510	2	08NTN9	Q8ntn9 corynebacte
33	37	64.9	671	2	08Q0U6	Q8q0u6 mechanosarc
34	36	63.2	113	2	06J4F4	Q6j4f4 neodiplo
35	36	63.2	175	2	07WNH8	Q7wnh8 bordetella
36	36	63.2	244	2	07VQO3	Q7vqo3 candidatus
37	36	63.2	284	2	08XGZ5	Q8xgz5 salmonella
38	36	63.2	284	2	07CPQ7	Q7cpq7 salmonella
39	36	63.2	301	2	07Q4C0	Q7q4c0 anophel
40	36	63.2	307	2	08LAW9	Q8law9 arabidopsi
41	36	63.2	307	2	067ZM1	Q67zm1 arabidopsi
42	36	63.2	307	2	067ZM1	Q67zm1 arabidopsi
43	36	63.2	337	1	Y6Z1_YEAST	Y6z1 yeast
44	36	63.2	349	2	09SRT5	Q9srt5 saccharomyc
45	36	63.2	379	2	0948E9	Q948e9 oryza sativ

ALIGNMENTS

RESULT 1
TF3B_SCHPO STANDARD; PRT; 500 AA.
AC Q9P6R0; Q9USU4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transcription factor IIB 60 kDa subunit (TFIIB) (B-related factor)
DE (BRF) (TFIIB-related factor).
GN Name=Brfl; ORFNames=SPBC13E7.10C, SPBC30D10.20;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Jones L., Jones M., Leathers S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volscheart G., Aert R., Robben J., Grymopoulos B.,
RA Wellens J., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinrich E., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Motier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Centuri L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shepkovskii G.V., Ussery D., Barrell B.G., Nuree P.,
RA "The genome sequence of Schizosaccharomyces pombe".
RL Nature 415:871-880(2002).
RN [2]
RP INTERACTION WITH TBP.
RX MEDLINE=22566152; PubMed=12682361; DOI=10.1093/nar/gkg301;
RA Huang Y., McGillicuddy E., Weinidel M., Dong S., Maria R.J.,
RA "The fission yeast TFIIB-related factor limits RNA polymerase III to a
RT TATA-dependent pathway of TBP recruitment".
RL Nucleic Acids Res. 31:2108-2116(2003).
CC -!- FUNCTION: General activator of RNA polymerase III transcription.
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 7.44134 Seconds
(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-17

Perfect score: 57

Sequence: 1 RRIKRIHIK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	68.4	202	1 H70318	conserved hypotet
2	39	68.4	210	2 AC1577	precocin isomeras
3	38	66.7	272	2 AB3430	transposase BME14
4	38	66.7	623	2 S73462	transport ATP-bind
5	37	64.9	87	2 S00180	spermatid protein
6	37	64.9	125	2 A99114	hypothetical prote
7	37	64.9	368	2 C69984	conserved hypotet
8	36	63.2	284	2 A10897	tagatose-bisphosph
9	36	63.2	317	2 S46010	hypothetical prote
10	36	63.2	569	2 C83952	prolyl-tRNA synth
11	36	63.2	613	2 F64056	probable ATP-depen
12	35	61.4	164	2 T50602	ribosomal protein
13	35	61.4	164	2 G86230	hypothetical prote
14	35	61.4	164	2 H96610	probable 60S ribos
15	35	61.4	212	2 A64045	2-dehydro-3-deoxy-
16	35	61.4	220	2 C53376	hypothetical prote
17	35	61.4	330	2 T22852	hypothetical prote
18	35	61.4	370	2 C70464	GTP-binding protei
19	35	61.4	381	2 F71078	hypothetical prote
20	35	61.4	522	2 T24144	hypothetical prote
21	35	61.4	529	1 XYECM	site-specific DNA-
22	35	61.4	532	2 T38326	serine threonine p
23	35	61.4	1258	2 T14855	reverse transcript
24	34	59.6	89	4 T46004	probable pseudogen
25	34	59.6	128	4 A12766	transcription regu
26	34	59.6	130	2 D97547	probable transcrip
27	34	59.6	253	2 S19409	probable membrane
28	34	59.6	253	2 D88338	protein P15A4.5 [1
29	34	59.6	283	2 A99284	hypothetical prote

30	34	59.6	306	2 E37471	hypothetical helic
31	34	59.6	352	2 H86454	CDS protein P9L11.
32	34	59.6	407	2 T37888	hypothetical prote
33	34	59.6	449	2 S16748	proline-rich prote
34	34	59.6	483	2 B82160	hypothetical prote
35	34	59.6	507	2 T10753	intestinal DNA rep
36	34	59.6	513	2 F90488	long-chain-fatty-a
37	34	59.6	590	2 C68099	protein P18A12.8 [
38	34	59.6	672	2 S46276	acetate-CoA ligase
39	34	59.6	699	2 G70142	DNA helicase (uvrD
40	34	59.6	773	2 H70108	hypothetical prote
41	34	59.6	780	2 AB1801	amino-terminal dom
42	34	59.6	867	2 G69485	DNA-directed RNA p
43	34	59.6	1012	2 S68259	DNA polymerase gam
44	34	59.6	1188	2 C71231	hypothetical prote
45	34	59.6	54	2 C90857	hypothetical prote

ALIGNMENTS

RESULT 1
H70318
conserved hypothetical protein aq_202 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: H70318
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; (V.)
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:9819666; PMID:9537320
A:Accession: H70318
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-202 <AQP>
A:Cross-references: UNIPROT:O66580; GB:AE00678; NID:92982921; PIDN:AC06551.1; PID:92;
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_202
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0226

Query Match 68.4%; Score 39; DB 1; Length 202;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRIKRIHIK 12
Db 186 RALRKLHVHLK 196

RESULT 2
AC1577
precocin isomerase homolog lin156 [imported] - Listeria innocua (strain Clj11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1577
R:Glaser, P.; Frangul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloecke
D.; Jones, L.M.; Karsel, U.
Science 294, 849-852, 2001
A:Authors: Krefl, U.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; W
ok, C.; Schleuter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A:Title: Comparative genomes of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1577
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <GLA>
A:Cross-references: UNIPROT:O92C45; GB:AL592022; PIDN:CAC96387.1; PID:g16413615; GSPDB:
A:Experimental source: strain Clj11262
C:Genetics:
A:Gene: lin156

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 32.648 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-17

Perfect score: 57

Sequence: 1 RRIIRKIHNIK 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	14	US-10-060-102-13	Sequence 13, Appl
2	57	100.0	14	US-10-060-102-18	Sequence 18, Appl
3	57	100.0	14	US-10-060-102-19	Sequence 19, Appl
4	57	100.0	14	US-10-060-102-20	Sequence 20, Appl
5	57	100.0	14	US-10-721-839-13	Sequence 13, Appl
6	57	100.0	14	US-10-721-839-18	Sequence 18, Appl
7	57	100.0	14	US-10-721-839-19	Sequence 19, Appl
8	57	100.0	14	US-10-721-839-20	Sequence 20, Appl
9	57	100.0	14	US-10-060-102-14	Sequence 14, Appl
10	57	100.0	16	US-10-060-102-15	Sequence 15, Appl
11	57	100.0	16	US-10-721-839-14	Sequence 14, Appl
12	57	100.0	16	US-10-721-839-15	Sequence 15, Appl
13	57	100.0	18	US-09-840-009-2	Sequence 2, Appl

14	57	100.0	18	9	US-09-840-009-9	Sequence 9, Appl
15	57	100.0	18	9	US-09-840-009-16	Sequence 16, Appl
16	57	100.0	18	9	US-09-840-009-23	Sequence 23, Appl
17	57	100.0	18	9	US-09-840-009-30	Sequence 30, Appl
18	57	100.0	18	14	US-10-060-102-9	Sequence 9, Appl
19	57	100.0	18	14	US-10-060-102-10	Sequence 10, Appl
20	57	100.0	18	14	US-10-060-102-11	Sequence 11, Appl
21	57	100.0	18	14	US-10-060-102-12	Sequence 12, Appl
22	57	100.0	18	15	US-10-721-839-9	Sequence 9, Appl
23	57	100.0	18	15	US-10-721-839-10	Sequence 10, Appl
24	57	100.0	18	15	US-10-721-839-11	Sequence 11, Appl
25	57	100.0	18	15	US-10-721-839-12	Sequence 12, Appl
26	57	100.0	29	15	US-10-060-102-8	Sequence 8, Appl
27	57	100.0	29	15	US-10-721-839-8	Sequence 8, Appl
28	52	91.2	18	9	US-09-840-009-8	Sequence 8, Appl
29	52	91.2	18	9	US-09-840-009-11	Sequence 11, Appl
30	52	91.2	18	9	US-09-840-009-15	Sequence 15, Appl
31	52	91.2	18	9	US-09-840-009-18	Sequence 18, Appl
32	52	91.2	18	9	US-09-840-009-22	Sequence 22, Appl
33	52	91.2	18	9	US-09-840-009-25	Sequence 25, Appl
34	52	91.2	18	9	US-10-060-102-25	Sequence 25, Appl
35	52	91.2	18	15	US-10-721-839-25	Sequence 25, Appl
36	52	91.2	18	15	US-10-721-839-25	Sequence 25, Appl
37	52	91.2	18	15	US-10-721-839-25	Sequence 25, Appl
38	51	89.5	18	9	US-09-840-009-5	Sequence 5, Appl
39	51	89.5	18	9	US-09-840-009-12	Sequence 12, Appl
40	51	89.5	18	9	US-09-840-009-19	Sequence 19, Appl
41	51	89.5	18	9	US-09-840-009-26	Sequence 26, Appl
42	50	87.7	18	9	US-09-840-009-6	Sequence 6, Appl
43	50	87.7	18	9	US-09-840-009-7	Sequence 7, Appl
44	50	87.7	18	9	US-09-840-009-13	Sequence 13, Appl
45	50	87.7	18	9	US-09-840-009-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-13
Sequence 13, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-13

Query Match 100.0%; Score 57; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR 1 RRIIRKIHNIK 12

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 11.3966 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-17

Perfect score: 57

Sequence: 1 RRIIRKIHNIK 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/aa/PTUS_COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfillseq1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	18	4	US-09-840-009-2
2	57	100.0	18	4	US-09-840-009-9
3	57	100.0	18	4	US-09-840-009-16
4	57	100.0	18	4	US-09-840-009-23
5	57	100.0	18	4	US-09-840-009-30
6	52	91.2	18	4	US-09-840-009-4
7	52	91.2	18	4	US-09-840-009-8
8	52	91.2	18	4	US-09-840-009-11
9	52	91.2	18	4	US-09-840-009-15
10	52	91.2	18	4	US-09-840-009-18
11	52	91.2	18	4	US-09-840-009-22
12	52	91.2	18	4	US-09-840-009-25
13	52	91.2	18	4	US-09-840-009-29
14	51	89.5	18	4	US-09-840-009-5
15	51	89.5	18	4	US-09-840-009-12
16	51	89.5	18	4	US-09-840-009-19
17	51	89.5	18	4	US-09-840-009-26
18	50	87.7	18	4	US-09-840-009-6
19	50	87.7	18	4	US-09-840-009-7
20	50	87.7	18	4	US-09-840-009-13
21	50	87.7	18	4	US-09-840-009-14
22	50	87.7	18	4	US-09-840-009-20
23	50	87.7	18	4	US-09-840-009-21
24	50	87.7	18	4	US-09-840-009-27
25	50	87.7	18	4	US-09-840-009-28
26	49	86.0	18	4	US-09-840-009-3
27	49	86.0	18	4	US-09-840-009-10

28	49	86.0	18	4	US-09-840-009-17	Sequence 17, Appl
29	49	86.0	18	4	US-09-840-009-24	Sequence 24, Appl
30	49	86.0	18	4	US-09-840-009-31	Sequence 31, Appl
31	49	86.0	18	4	US-09-840-009-34	Sequence 34, Appl
32	49	86.0	18	4	US-09-840-009-35	Sequence 35, Appl
33	41	71.9	18	4	US-09-840-009-32	Sequence 32, Appl
34	41	71.9	18	4	US-09-840-009-33	Sequence 33, Appl
35	41	71.9	18	4	US-09-840-009-36	Sequence 36, Appl
36	41	71.9	18	4	US-09-840-009-37	Sequence 37, Appl
37	37	64.9	18	4	US-09-840-009-1	Sequence 1, Appl
38	37	64.9	18	4	US-09-840-009-3	Sequence 3, Appl
39	37	64.9	18	4	US-09-840-009-5	Sequence 5, Appl
40	37	64.9	18	4	US-09-840-009-6	Sequence 6, Appl
41	37	64.9	18	4	US-09-840-009-7	Sequence 7, Appl
42	37	64.9	18	4	US-09-840-009-8	Sequence 8, Appl
43	37	64.9	18	4	US-09-840-009-9	Sequence 9, Appl
44	36	63.2	18	4	US-09-840-009-10	Sequence 10, Appl
45	36	63.2	18	4	US-09-840-009-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2

Sequence 2, Application US/09840009

Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.

TITLE OF INVENTION: NOVIPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0

CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match
Best Local Similarity 100.0%; Score 57; DB 4; Length 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRIIRKIHNIK 12
DB 4 RRIIRKIHNIK 15

RESULT 2
US-09-840-009-9

Sequence 9, Application US/09840009

Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.

TITLE OF INVENTION: NOVIPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0

CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 / Search time 42.067 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-17

Perfect score: 57

Sequence: 1 RRIIRKIHNIK 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04.*

1: geneseqp19808.*
2: geneseqp19808.*
3: geneseqp20008.*
4: geneseqp20018.*
5: geneseqp20028.*
6: geneseqp20038.*
7: geneseqp20038.*
8: geneseqp20048.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	12	4	AAB70664
2	57	100.0	13	4	AAB70662
3	57	100.0	13	4	AAB70663
4	57	100.0	14	4	AAB70658
5	57	100.0	14	4	AAB70659
6	57	100.0	14	4	AAB70661
7	57	100.0	14	4	AAB70660
8	57	100.0	14	5	ABP53286
9	57	100.0	14	5	ABP53280
10	57	100.0	14	5	ABP53287
11	57	100.0	14	5	ABP53285
12	57	100.0	16	4	AAB70656
13	57	100.0	16	4	AAB70657
14	57	100.0	16	5	ABP53282
15	57	100.0	16	5	ABP53281
16	57	100.0	18	4	AAB70655
17	57	100.0	18	4	AAB70648
18	57	100.0	18	5	AAB70654
19	57	100.0	18	5	AAB70652
20	57	100.0	18	5	AAB70654
21	57	100.0	18	5	AAB70654
22	57	100.0	18	5	AAB70654
23	57	100.0	18	5	AAB70654
24	57	100.0	18	5	AAB70654
25	57	100.0	18	5	AAB70654

26	57	100.0	18	5	ABP53277	Abp53277 Synthetic
27	57	100.0	18	5	ABP53279	Abp53279 Synthetic
28	57	100.0	20	4	AAB70653	Aab70653 Ovine SMA
29	57	100.0	29	4	AAB70675	Abp70675 Ovine SMA
30	57	100.0	29	5	ABP53275	Abp53275 Synthetic
31	52	91.2	18	5	AAB70680	Aae20870 T10-nov18
32	52	91.2	18	5	AAB70680	Aae20860 D16-nov18
33	52	91.2	18	5	AAB70681	Aae20881 D11-nov18
34	52	91.2	18	5	AAB70681	Aae20867 DA7-nov18
35	52	91.2	18	5	AAB70687	Aae20874 DA10-nov18
36	52	91.2	18	5	AAB70683	Aae20863 T7-nov18
37	52	91.2	18	5	AAB70687	Aae20877 T11-nov18
38	52	91.2	18	5	AAB70686	Aae20856 T6-nov18
39	52	91.2	18	5	ABP53292	Abp53292 Synthetic
40	51	89.5	18	5	AAB70684	Aae20864 S7-nov18
41	51	89.5	18	5	AAB70681	Aae20871 S10-nov18
42	51	89.5	18	5	AAB70687	Aae20878 S11-nov18
43	51	89.5	18	5	AAB70687	Aae20857 S6-nov18
44	50	87.7	18	5	AAB70682	Aae20872 E10-nov18
45	50	87.7	18	5	AAB70673	Aae20873 D10-nov18

ALIGNMENTS

RESULT 1

AAB70664 ID AAB70664 standard; peptide; 12 AA.

XX AAB70664;

DT 15-MAY-2001 (first entry)

DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:17.

XX Ovine: SNAP29; lupine: RCAP 18; cathelicidin; antimicrobial;

KM bactericidal; antibiotic; antiviral; microbial growth inhibitor;

KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

XX Burkholderia cepacia; Alcaligenes; Xanthomonas.

OS Ovis aries.

XX WO200112668-A1.

PN 22-FEB-2001.

PF 18-AUG-2000; 2000WO-US022781.

PR 18-AUG-1999; 99US-0149886P.

PA (IOWA) UNIV IOWA RES FOUND.

XX (REGC) UNIV CALIFORNIA.

PI Tack BE, Mccravy P, Welsh M, Travis SM, Lehrer R;

XX WPI; 2001-234911/24.

PT New antimicrobial peptides useful as antibiotics for inhibiting growth

XX and proliferation of microbes, and for treating microbial infections.

PS Claim 1; Page 103; 137p; English.

CC AAB70648 to AAB70675 represent antimicrobial peptides (1), of which

CC SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived

CC from the lupine RCAP 18 cathelicidin family peptide. (1) have antibiotic,

CC antimicrobial and antiviral activities, and can be used as microbial

CC growth and proliferation inhibitors and in gene therapy. (1) are useful

CC for inhibiting microbial growth in an environment capable of sustaining

CC such growth, for inhibiting microbial growth or strain in a host, and

CC inhibiting the growth of drug-resistant microbial strains such as

CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 40.5615 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-16
Perfect score: 62
Sequence: 1 RRIKRIHIIKK 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	69.4	638	2	Q8D796
2	43	69.4	660	2	Q7MEAO
3	42	67.7	125	2	Q9AVZ1
4	42	67.7	308	2	Q8R2C7
5	42	67.7	500	1	TF3B_SCHPO
6	41	66.1	337	1	YB21_YEAST
7	41	66.1	414	2	Q947U2
8	41	66.1	613	1	Q7XEY8
9	41	66.1	613	1	DEAD_HAETN
10	41	66.1	670	1	REP_BUCBP
11	40	64.5	256	2	Q83CP2
12	40	64.5	370	2	Q67743
13	40	64.5	452	2	Q7N787
14	40	64.5	475	2	Q75G18
15	39	62.9	202	1	HAM1_AQUAE
16	39	62.9	210	2	Q92C15
17	39	62.9	250	2	Q7W5F0
18	39	62.9	250	2	Q7W5F0
19	39	62.9	258	2	Q8MY71
20	39	62.9	407	2	Q9UTH1
21	39	62.9	461	2	Q81BM2
22	39	62.9	483	2	Q9KR81
23	39	62.9	598	2	Q7VTH0
24	39	62.9	967	2	Q28391
25	39	62.9	1157	2	Q7R0N5
26	39	62.9	1157	2	Q7R0N5
27	39	62.9	4057	2	Q81U57
28	38	61.3	87	1	SSS1_SCYCA
29	38	61.3	160	1	SCS1_SHEEP
30	38	61.3	160	1	SCS1_SHEEP
31	38	61.3	262	2	Q720G5

32	38	61.3	272	2	Q8YFUG	Q8YFUG bruceella me
33	38	61.3	415	2	Q8SPU4	Q8SPU4 nicotiana t
34	38	61.3	428	2	Q8TXS5	Q8TXS5 methanopyru
35	38	61.3	457	1	BAG4_HUMAN	BAG4_HUMAN
36	38	61.3	457	1	BAG4_MOUSE	BAG4_MOUSE
37	38	61.3	491	2	Q9H8X2	Q9H8X2 homo sapien
38	38	61.3	574	2	SYP_BUCBP	SYP_BUCBP
39	38	61.3	623	1	Y014_MYCPN	Y014_MYCPN
40	38	61.3	636	2	Q87HT7	Q87HT7 mycoplasma
41	38	61.3	670	1	REP_HAETN	REP_HAETN
42	38	61.3	834	2	Q7RR10	Q7RR10 haemophilus
43	38	61.3	878	2	Q7RY40	Q7RY40 plasmodium
44	37	59.7	41	2	Q48971	Q48971 neurospora
45	37	59.7	207	2	Q846Q4	Q846Q4 myxococcus

ALIGNMENTS

RESULT 1

ID	Q8D796	PRELIMINARY;	PRT;	638 AA.
AC	Q8D796;			
DT	01-MAR-2003 (T-EMBLrel. 23, Created)			
DT	01-MAR-2003 (T-EMBLrel. 23, Last sequence update)			
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)			
DE	Predicted signal transduction protein.			
GN	OrderedLocusNames=V20264;			
OS	Vibrio vulnificus.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;			
OC	Vibrionaceae; Vibrio.			
OX	NCBI_Taxid=672;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CMCP6;			
RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,			
RT	Choy H.E.;			
RL	*Complete genome sequence of Vibrio vulnificus CMCP6.*/			
DR	Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AB016808; AA007230.1; -			
DR	InterPro; IPR001633; EAL.			
DR	InterPro; IPR003018; GAF.			
DR	InterPro; IPR000160; GGDEF.			
DR	Pfam; PF00563; EAL; 1.			
DR	Pfam; PF00590; GAF; 1.			
DR	Pfam; PF00990; GGDEF; 1.			
DR	SMART; SM00052; DUF2; 1.			
DR	SMART; SM00065; GAF; 1.			
DR	TIGRFAMs; TIGR00254; GGDEF; 1.			
DR	PROSITE; PS50883; EAL; 1.			
DR	PROSITE; PS50887; GGDEF; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64;			
Qy	1 RRIKRIHIIKK 13			
Db	566 KEIRRSIIHAKK 578			
Query Match	69.4%;	Score 43;	DB 2;	Length 638;
Best Local Similarity	61.5%;	Pred. No. 41;		
Matches	8; Conservative	2; Mismatches	3; Indels	0; Gaps 0;
RESULT 2				
ID	Q7MEAO	PRELIMINARY;	PRT;	660 AA.
AC	Q7MEAO;			
DT	01-MAR-2004 (T-EMBLrel. 26, Created)			
DT	01-MAR-2004 (T-EMBLrel. 26, Last sequence update)			
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)			
DE	GGDEF family protein.			
GN	OrderedLocusNames=VVA0770;			
OS	Vibrio vulnificus (strain Y016).			

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.06145 Seconds

(without alignment)
155.160 Million cell updates/sec

Title: US-09-642-744D-16

Perfect score: 62

Sequence: 1 RRIIRKIIHIKK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 79: *

1: PIR1: *

2: PIR2: *

3: PIR3: *

4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	67.7	125	2 A99114	hypothetical prote
2	41	66.1	337	2 S46010	hypothetical prote
3	41	66.1	613	2 F64056	probable ATP-depen
4	40	64.5	370	2 C70464	GTP-binding protei
5	39	62.9	202	1 H70318	conserved hypochet
6	39	62.9	210	2 AC1577	precortin isomeras
7	39	62.9	407	2 T37688	hypothetical prote
8	39	62.9	483	2 B82160	hypothetical prote
9	39	62.9	867	2 G69485	DNA-directed RNA p
10	38	61.3	87	2 S00180	spermatid protein
11	38	61.3	152	2 S68411	catheilin-related p
12	38	61.3	160	2 S68412	myeloid antimicrob
13	38	61.3	150	2 S68228	transposase BME114
14	38	61.3	272	2 AB3430	transport ATP-bind
15	38	61.3	623	2 S73462	helicase (RC 3.6.1
16	38	61.3	698	2 D64084	hypothetical prote
17	37	59.7	41	2 S77768	endoglycanase - Th
18	37	59.7	334	2 B72301	conserved hypochet
19	37	59.7	368	2 C69884	prolyl-tRNA synthet
20	37	59.7	559	2 C83952	hypothetical prote
21	36	58.1	117	2 T12722	tagatose-bisphosph
22	36	58.1	284	2 A10897	hypothetical prote
23	36	58.1	299	2 A10897	hypothetical prote
24	36	58.1	310	2 A33489	hypothetical prote
25	36	58.1	370	2 A05034	hypothetical prote
26	36	58.1	447	2 P81678	GTP-binding protei
27	36	58.1	499	2 G84972	leucyl aminopeptid
28	36	58.1	627	2 C82418	GGDP family prote
29	36	58.1	760	2 T24521	hypothetical prote

30	35	56.5	128	2 A12766	transcription regu
31	35	56.5	128	2 D97547	probable transcrip
32	35	56.5	164	2 T50602	ribosomal protein
33	35	56.5	164	2 G86230	hypothetical prote
34	35	56.5	164	2 H96610	probable 60S ribos
35	35	56.5	212	2 A64045	2-dehydro-3-deoxy-
36	35	56.5	220	2 C53376	hypothetical prote
37	35	56.5	222	2 F72572	probable TAPA-box
38	35	56.5	330	2 T22852	hypothetical prote
39	35	56.5	381	2 F71078	hypothetical prote
40	35	56.5	414	2 G71331	probable cell divi
41	35	56.5	420	2 E72357	sugar ABC transpor
42	35	56.5	420	2 S45630	DNA primase chain
43	35	56.5	436	2 G97186	diverged glycosylc
44	35	56.5	491	2 AC1185	B. subtilis YDB p
45	35	56.5	494	2 AB1543	B. subtilis YDB p

ALIGNMENTS

RESULT 1

A99114 hypothetical protein orf125 [imported] - Guillardia theta nucleomorph

C/Species: nucleomorph Guillardia theta

A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: A99114

R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001

A/Title: The highly reduced genome of an enslaved algal nucleus.

A/Reference number: A99082; NCBI:11323671; PMID:11323671

A/Accession: A99114

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-125 <DOU>

A/Cross-references: UNIPROT:Q9AVZ1; GB:AJ010592; NID:G12580762; PIDN:CAC27080.1; GSPDB:

C/Genetics:

A/Map position: 2

A/Genome: nucleomorph

C/Keywords: nucleomorph

Query Match 67.7%; Score 42; DB 2; Length 125;

Best Local Similarity 70.0%; Pred. No. 4.4;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 IRKIIHIKK 13

DB 9 IRKIIHLVRK 18

RESULT 2

S46010 hypothetical protein YBR141c - Yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YBR1118

C/Species: Saccharomyces cerevisiae

C/Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C/Accession: S46010

R/Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.

submitted to the Protein Sequence Database, August 1994

A/Reference number: S45995

A/Accession: S46010

A/Molecule type: DNA

A/Residues: 1-337 <BEC>

A/Cross-references: UNIPROT:P38278; EMBL:Z36010; NID:G536439; PID:G536440; GSPDB:GN0000

A/Experimental source: strain S288C

C/Genetics:

A/Map position: 2R

Query Match 66.1%; Score 41; DB 2; Length 337;

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 12.3464 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-16

Perfect score: 62

Sequence: 1 RRIIRKIHIIKK 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	18	4	US-09-840-009-2
2	62	100.0	18	4	US-09-840-009-9
3	62	100.0	18	4	US-09-840-009-16
4	62	100.0	18	4	US-09-840-009-23
5	62	100.0	18	4	US-09-840-009-30
6	57	91.9	18	4	US-09-840-009-4
7	57	91.9	18	4	US-09-840-009-8
8	57	91.9	18	4	US-09-840-009-11
9	57	91.9	18	4	US-09-840-009-15
10	57	91.9	18	4	US-09-840-009-18
11	57	91.9	18	4	US-09-840-009-22
12	57	91.9	18	4	US-09-840-009-25
13	57	91.9	18	4	US-09-840-009-29
14	56	90.3	18	4	US-09-840-009-5
15	56	90.3	18	4	US-09-840-009-12
16	56	90.3	18	4	US-09-840-009-19
17	56	90.3	18	4	US-09-840-009-26
18	55	88.7	18	4	US-09-840-009-6
19	55	88.7	18	4	US-09-840-009-7
20	55	88.7	18	4	US-09-840-009-13
21	55	88.7	18	4	US-09-840-009-14
22	55	88.7	18	4	US-09-840-009-20
23	55	88.7	18	4	US-09-840-009-21
24	55	88.7	18	4	US-09-840-009-27
25	55	88.7	18	4	US-09-840-009-28
26	54	87.1	18	4	US-09-840-009-3
27	54	87.1	18	4	US-09-840-009-10

28	54	87.1	18	4	US-09-840-009-17	Sequence 17, Appl
29	54	87.1	18	4	US-09-840-009-24	Sequence 24, Appl
30	54	87.1	18	4	US-09-840-009-31	Sequence 31, Appl
31	54	87.1	18	4	US-09-840-009-34	Sequence 34, Appl
32	54	87.1	18	4	US-09-840-009-35	Sequence 35, Appl
33	46	74.2	18	4	US-09-840-009-32	Sequence 32, Appl
34	46	74.2	18	4	US-09-840-009-33	Sequence 33, Appl
35	46	74.2	18	4	US-09-840-009-36	Sequence 36, Appl
36	46	74.2	18	4	US-09-840-009-37	Sequence 37, Appl
37	42	67.7	18	4	US-09-840-009-1	Sequence 1, Appl
38	41	66.1	337	4	US-09-538-092-38	Sequence 38, Appl
39	39	62.9	24	4	US-09-785-0598-5	Sequence 5, Appl
40	39	62.9	36	4	US-09-785-0598-6	Sequence 6, Appl
41	39	62.9	42	4	US-09-785-0598-7	Sequence 7, Appl
42	39	62.9	48	4	US-09-785-0598-8	Sequence 8, Appl
43	38	61.3	149	4	US-09-774-639-304	Sequence 104, App
44	38	61.3	160	4	US-09-917-340-36	Sequence 36, App
45	38	61.3	229	4	US-09-394-1428-8	Sequence 8, Appl

ALIGNMENTS

```
RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Robert I.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606, 858
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          100.0%; Score 62; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 RRIIRKIHIIKK 13
         |||||
Db       4 RRIIRKIHIIKK 16

RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Robert I.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606, 858
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 45.5726 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-16
Perfect score: 62
Sequence: 1 RRIIRKIHICK 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	13	4 AAB70663	Aab70663 Ovine SMA
2	62	100.0	14	4 AAB70658	Aab70658 Ovine SMA
3	62	100.0	14	4 AAB70659	Aab70659 Ovine SMA
4	62	100.0	14	4 AAB70661	Aab70661 Ovine SMA
5	62	100.0	14	4 AAB70660	Aab70660 Ovine SMA
6	62	100.0	14	4 AAB70657	Aab70657 Ovine SMA
7	62	100.0	14	4 AAB70656	Aab70656 Ovine SMA
8	62	100.0	14	4 AAB70655	Aab70655 Ovine SMA
9	62	100.0	14	4 AAB70654	Aab70654 Ovine SMA
10	62	100.0	14	4 AAB70653	Aab70653 Ovine SMA
11	62	100.0	14	4 AAB70652	Aab70652 Ovine SMA
12	62	100.0	14	4 AAB70651	Aab70651 Ovine SMA
13	62	100.0	14	4 AAB70650	Aab70650 Ovine SMA
14	62	100.0	14	4 AAB70649	Aab70649 Ovine SMA
15	62	100.0	14	4 AAB70648	Aab70648 Ovine SMA
16	62	100.0	14	4 AAB70647	Aab70647 Ovine SMA
17	62	100.0	14	4 AAB70646	Aab70646 Ovine SMA
18	62	100.0	14	4 AAB70645	Aab70645 Ovine SMA
19	62	100.0	14	4 AAB70644	Aab70644 Ovine SMA
20	62	100.0	14	4 AAB70643	Aab70643 Ovine SMA
21	62	100.0	14	4 AAB70642	Aab70642 Ovine SMA
22	62	100.0	14	4 AAB70641	Aab70641 Ovine SMA
23	62	100.0	14	4 AAB70640	Aab70640 Ovine SMA
24	62	100.0	14	4 AAB70639	Aab70639 Ovine SMA
25	62	100.0	14	4 AAB70638	Aab70638 Ovine SMA

25	62	100.0	20	4 AAB70653	Aab70653 Ovine SMA
27	62	100.0	29	4 AAB70675	Aab70675 Ovine SMA
28	62	100.0	29	4 AAB70675	Aab70675 Ovine SMA
29	62	100.0	29	4 AAB70675	Aab70675 Ovine SMA
30	57	91.9	12	4 AAB70664	Aab70664 Ovine SMA
31	57	91.9	13	4 AAB70662	Aab70662 Ovine SMA
32	57	91.9	18	5 AAB70670	Aab70670 Ovine SMA
33	57	91.9	18	5 AAB70680	Aab70680 Ovine SMA
34	57	91.9	18	5 AAB70681	Aab70681 Ovine SMA
35	57	91.9	18	5 AAB70687	Aab70687 Ovine SMA
36	57	91.9	18	5 AAB70686	Aab70686 Ovine SMA
37	57	91.9	18	5 AAB70685	Aab70685 Ovine SMA
38	57	91.9	18	5 AAB70684	Aab70684 Ovine SMA
39	57	91.9	18	5 AAB70683	Aab70683 Ovine SMA
40	56	90.3	18	5 AAB70682	Aab70682 Ovine SMA
41	56	90.3	18	5 AAB70681	Aab70681 Ovine SMA
42	56	90.3	18	5 AAB70680	Aab70680 Ovine SMA
43	56	90.3	18	5 AAB70679	Aab70679 Ovine SMA
44	56	90.3	18	5 AAB70678	Aab70678 Ovine SMA
45	55	88.7	18	5 AAB70677	Aab70677 Ovine SMA

ALIGNMENTS

RESULT 1	AAB70663	standard; peptide; 13 AA.
ID	AAB70663	
AC	AAB70663	
XX		
DT	15-MAY-2001 (first entry)	
DE	Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:16.	
XX		
KW	Ovine: SNAP29, Iupine: RCAP 18, cathelicidin; antimicrobial; bactericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Xanthomonas.	
KW	Burkholderia cepacia; Alcaligenes; Xanthomonas.	
OS	Ovis aries.	
XX		
PN	WO200112668-A1.	
XX		
PD	22-FEB-2001.	
XX		
PF	18-AUG-2000; 2000WO-US022781.	
XX		
PR	18-AUG-1999; 99US-0149886P.	
XX		
PA	(IOWA) UNIV IOWA RES FOUND.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Tack BE, McCreary P, Welsh M, Travis SM, Lehrer R, WPI; 2001-234911/24.	
XX		
DR		
XX		
PT	New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections.	
XX		
PS	Claim 1, Page 103, 137pp, English.	
XX		
CC	AAB70648 to AAB70675 represent antimicrobial peptides (I), of which SNAP 29 cathelicidin family peptide, and AAB70675 are derived from the ovine antimicrobial and antiviral activites, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (I) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas	

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 40.5615 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: us-09-642-744d-15

Perfect score: 61

Sequence: 1 LRRIRKIHNIK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68.9	500	1	TF3B_SCHPO	Q9P6T0 echinosacch
2	67.2	670	1	REP_BUCBP	Q99A21 buchiera ap
3	65.6	414	2	Q94702	Q94702 oryza sativ
4	65.6	414	2	Q7XEX8	Q7XEX8 oryza sativ
5	63.9	202	1	HAM1_AQUAE	Q66580 aquilex aeo
6	63.9	210	2	Q92C15	Q92C15 listeria in
7	63.9	4057	2	Q81UE7	Q81UE7 plasmodium
8	63.9	250	2	Q7W5F0	Q7W5F0 bordetella
9	62.3	250	2	Q7W5F0	Q7W5F0 bordetella
10	62.3	262	2	Q72005	Q72005 phlebotomus
11	62.3	272	2	Q8YF06	Q8YF06 brucella me
12	62.3	284	2	Q8XGZ9	Q8XGZ9 salmonella
13	62.3	284	2	Q7C907	Q7C907 salmonella
14	62.3	428	2	Q8TXS5	Q8TXS5 methanopyru
15	62.3	475	1	GATB_THETN	Q8XC39 thermoanaer
16	62.3	475	1	GATB_THETN	Q8XC39 thermoanaer
17	62.3	574	1	SYP_BUCBP	Q89A21 buchiera ap
18	62.3	598	2	Q7VTH0	Q7VTH0 bordetella
19	62.3	633	1	Y014_MYCPN	P75055 mycoplasma
20	62.3	638	2	Q8D796	Q8D796 vibrio vuln
21	62.3	660	2	Q7MEA0	Q7MEA0 methanosc
22	62.3	671	2	Q8Q0U6	Q8Q0U6 methanosc
23	62.3	684	2	Q7QNN1	Q7QNN1 giardia lam
24	62.3	780	2	Q926T7	Q926T7 listeria in
25	62.3	838	2	Q9DVL4	Q9DVL4 human immun
26	62.3	862	2	Q8AUB9	Q8AUB9 human immun
27	62.3	878	2	Q7RY40	Q7RY40 neurospora
28	62.3	954	2	Q9GQ15	Q9GQ15 giardia lam
29	62.3	969	2	Q9U022	Q9U022 giardia lam
30	62.3	1157	2	Q7R0N5	Q7R0N5 plasmodium
31	62.3	1168	2	Q57849	Q57849 pyrococcus

32	37	60.7	87	1	SSS1_SCYCA	P13275 scyllorhinu
33	37	60.7	125	2	Q9AVZ1	Q9AVZ1 giardia
34	37	60.7	151	2	Q8R891	Q8R891 thermoanaer
35	37	60.7	160	1	SCS1_SHEEP	P49928 ovis aries
36	37	60.7	160	1	SCS2_SHEEP	P49929 ovis aries
37	37	60.7	207	2	Q846Q4	Q846Q4 myxococcus
38	37	60.7	295	2	Q13635	Q13635 schizosacch
39	37	60.7	301	2	Q86FM8	Q86FM8 caenorhabd
40	37	60.7	302	2	Q81126	Q81126 caenorhabd
41	37	60.7	328	2	Q8R2C7	Q8R2C7 mus musculu
42	37	60.7	352	2	Q9MAP0	Q9MAP0 arabidopsis
43	37	60.7	354	1	H181_OCEIH	Q8683 oceanobact
44	37	60.7	368	1	Y5F8_BACSU	P94536 bacillus su
45	37	60.7	415	2	Q9SPU4	Q9SPU4 nicotiana t

ALIGNMENTS

RESULT 1
TF3B_SCHPO STANDARD; PRT; 500 AA.
AC Q9P6T0; Q9USU4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transcription factor IIB 60 kDa subunit (TFIIB) (B-related factor)
DE 1 (BRF) (TFIIB-related factor)
GN Name=Brf1; ORFNames=SPBC1387.10c, SPBC30D10.20;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RX Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B., Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Medler H., Wambut S., Purrelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Leleaux V., Motter S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garcon A., Rhode G., Daga R.R., Cruzado L., Jimenez J., Sanchez S., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
RN Nature 415:871-880(2002).
RP INTERACTION WITH TBP.
RX MEDLINE=2269152; PubMed=12682361; DOI=10.1093/nar/gk9301;
RA Huang Y., McGillicuddy E., Weindel M., Dong S., Marata R.J.;
RT "The fission yeast TFIIB-related factor limits RNA polymerase III to a TBP-dependent pathway of TBP recruitment.";
RL Nucleic Acids Res. 31:2108-2116(2003).
CC -I- FUNCTION: General activator of RNA polymerase III transcription.
CC -I- COPACITOR: Binds 1 zinc ion per subunit (By similarity).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.06145 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-15

Perfect score: 61

Sequence: 1 LRRIIRKIHNIK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	63.9	202	1 H70318	conserved hypochet
2	39	63.9	210	2 AC1577	precortin isomeras
3	38	62.3	272	2 AB3430	transposase BMR14
4	38	62.3	284	2 A10897	regucalcin-bisphosph
5	38	62.3	623	2 S73462	transport ATP-bind
6	38	62.3	780	2 AB1801	amino-terminal dom
7	38	62.3	1188	2 C71231	hypothetical prote
8	37	60.7	87	2 S00180	spermatid protein
9	37	60.7	125	2 A99114	hypothetical prote
10	37	60.7	152	2 S68412	cathelin-related p
11	37	60.7	160	2 S68412	cathelin-related p
12	37	60.7	160	2 S68412	cathelin-related p
13	37	60.7	352	2 H86454	myeloid antimicrob
14	37	60.7	368	2 C69984	CDS protein F911.
15	36	59.0	41	2 S77768	conserved hypochet
16	36	59.0	337	2 S46010	hypothetical prote
17	36	59.0	357	2 S21992	hypothetical prote
18	36	59.0	484	2 A70558	envelope protein g
19	36	59.0	569	2 C83952	hypothetical prote
20	36	59.0	613	2 F64056	prolyl-tRNA synthet
21	36	59.0	672	2 S46276	probable ATP-depen
22	36	59.0	780	2 A11427	acetate-CoA ligase
23	36	59.0	8243	2 T31307	transcription regu
24	35	57.4	62	1 R5BS1F	type I fatty acid
25	35	57.4	155	2 AD1883	ribosomal protein
26	35	57.4	164	2 T50602	hypothetical prote
27	35	57.4	164	2 G86230	ribosomal protein
28	35	57.4	164	2 H96610	hypothetical prote
29	35	57.4	180	2 S39775	probable 60S ribos
					alpha-82-casein to

30	35	57.4	212	2 A64045	2-dehydro-3-deoxy-
31	35	57.4	220	2 C53376	hypothetical prote
32	35	57.4	330	2 T22852	hypothetical prote
33	35	57.4	356	2 T31851	hypothetical prote
34	35	57.4	370	2 C70464	GTP-binding protei
35	35	57.4	381	2 F71078	hypothetical prote
36	35	57.4	437	2 C86435	hypothetical prote
37	35	57.4	483	2 S75369	protein F178.15 l
38	35	57.4	519	2 B88322	hypothetical prote
39	35	57.4	519	2 T19998	protein C47D12.8 l
40	35	57.4	522	2 T24144	hypothetical prote
41	35	57.4	529	1 XIECHM	hypothetical prote
42	35	57.4	532	2 T38326	site-specific DNA-
43	35	57.4	577	2 F64549	serine threonine p
44	35	57.4	622	2 E72754	proline-tRNA ligas
45	35	57.4	626	1 SYNCA	probable phosphoen
					acetate-CoA ligase

ALIGNMENTS

RESULT 1

H70318 conserved hypothetical protein aq_202 - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004

C/Accession: H70318

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C

V. Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; PMID:98196666; PMID:9537320

A/Accession: H70318

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-202 <NOFS>

A/Cross-references: UNIPROT:O66580; GB:AE000678; NID:G2982921; PIDN:AA06551.1; PID:G25

A/Experimental source: strain VFS

C/Genetics:

A/Gene: aq_202

C/Superfamily: Methanococcus jannaschii conserved hypothetical protein M0226

Query Match

Best Local Similarity 63.9%; Score 39; DB 1; Length 202;

Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 RIRKIHNIK 13

DB 186 RLRKLVHVK 196

RESULT 2

AC1577 precortin isomerase homolog lin1156 [imported] - Listeria innocua (strain C11p11262)

C/Species: Listeria innocua

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #ext_change 09-Jul-2004

C/Accession: AC1577

R/Glaeser, P.; Frangoul, L.; Buchteler, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehrl, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kref, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; M

ok, C.; Schluter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland

A/Title: Comparative genomics of Listeria species

A/Reference number: AB1077; PMID:21537279; PMID:11679669

A/Accession: AC1577

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-210 <GLA>

A/Cross-references: UNIPROT:Q92CL5; GB:AL592022; PIDN:CA06387.1; PID:gl6413615; GSPDB:

C/Genetics:

A/Gene: lin1156

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 35.3687 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-15

Sequence: 1 LRRIRKIHIIK 13

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	14	US-10-060-102-13	Sequence 13, Appl
2	61	100.0	14	US-10-060-102-18	Sequence 18, Appl
3	61	100.0	14	US-10-721-839-13	Sequence 13, Appl
4	61	100.0	14	US-10-721-839-18	Sequence 18, Appl
5	61	100.0	16	US-10-060-102-14	Sequence 14, Appl
6	61	100.0	16	US-10-721-839-14	Sequence 14, Appl
7	61	100.0	18	US-09-840-009-2	Sequence 2, Appl
8	61	100.0	18	US-09-840-009-9	Sequence 9, Appl
9	61	100.0	18	US-09-840-009-15	Sequence 15, Appl
10	61	100.0	18	US-09-840-009-23	Sequence 23, Appl
11	61	100.0	18	US-09-840-009-30	Sequence 30, Appl
12	61	100.0	18	US-10-060-102-9	Sequence 9, Appl
13	61	100.0	18	US-10-060-102-12	Sequence 12, Appl

14	61	100.0	18	US-10-721-839-9	Sequence 9, Appl
15	61	100.0	18	US-10-721-839-12	Sequence 12, Appl
16	61	100.0	29	US-10-060-102-8	Sequence 8, Appl
17	61	100.0	29	US-10-721-839-8	Sequence 8, Appl
18	59	96.7	14	US-10-060-102-19	Sequence 19, Appl
19	59	96.7	14	US-10-060-102-20	Sequence 20, Appl
20	59	96.7	14	US-10-721-839-19	Sequence 19, Appl
21	59	96.7	14	US-10-721-839-20	Sequence 20, Appl
22	59	96.7	16	US-10-060-102-15	Sequence 15, Appl
23	59	96.7	16	US-10-721-839-15	Sequence 15, Appl
24	59	96.7	18	US-10-060-102-10	Sequence 10, Appl
25	59	96.7	18	US-10-060-102-11	Sequence 11, Appl
26	59	96.7	18	US-10-721-839-10	Sequence 10, Appl
27	59	96.7	18	US-10-721-839-11	Sequence 11, Appl
28	56	91.8	18	US-09-840-009-4	Sequence 4, Appl
29	56	91.8	18	US-09-840-009-11	Sequence 11, Appl
30	56	91.8	18	US-09-840-009-15	Sequence 15, Appl
31	56	91.8	18	US-09-840-009-18	Sequence 18, Appl
32	56	91.8	18	US-09-840-009-22	Sequence 22, Appl
33	56	91.8	18	US-09-840-009-25	Sequence 25, Appl
34	56	91.8	18	US-09-840-009-29	Sequence 29, Appl
35	56	91.8	18	US-10-060-102-25	Sequence 25, Appl
36	56	91.8	18	US-10-721-839-25	Sequence 25, Appl
37	56	91.8	18	US-09-840-009-5	Sequence 5, Appl
38	55	90.2	18	US-09-840-009-12	Sequence 12, Appl
39	55	90.2	18	US-09-840-009-19	Sequence 19, Appl
40	55	90.2	18	US-09-840-009-26	Sequence 26, Appl
41	55	90.2	18	US-09-840-009-6	Sequence 6, Appl
42	54	88.5	18	US-09-840-009-7	Sequence 7, Appl
43	54	88.5	18	US-09-840-009-13	Sequence 13, Appl
44	54	88.5	18	US-09-840-009-14	Sequence 14, Appl
45	54	88.5	18	US-09-840-009-13	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-13
; Sequence 13, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 13
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-13

Query Match 100.0%; Score 61; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRRIRKIHIIK 13

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 12.3464 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-15
Perfect score: 61
Sequence: 1 LRRIRKIHIIK 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	18	4	US-09-840-009-2
2	61	100.0	18	4	US-09-840-009-9
3	61	100.0	18	4	US-09-840-009-16
4	61	100.0	18	4	US-09-840-009-23
5	61	100.0	18	4	US-09-840-009-30
6	56	91.8	18	4	US-09-840-009-4
7	56	91.8	18	4	US-09-840-009-8
8	56	91.8	18	4	US-09-840-009-11
9	56	91.8	18	4	US-09-840-009-15
10	56	91.8	18	4	US-09-840-009-18
11	56	91.8	18	4	US-09-840-009-22
12	56	91.8	18	4	US-09-840-009-25
13	56	91.8	18	4	US-09-840-009-29
14	55	90.2	18	4	US-09-840-009-5
15	55	90.2	18	4	US-09-840-009-12
16	55	90.2	18	4	US-09-840-009-19
17	55	90.2	18	4	US-09-840-009-26
18	54	88.5	18	4	US-09-840-009-6
19	54	88.5	18	4	US-09-840-009-7
20	54	88.5	18	4	US-09-840-009-13
21	54	88.5	18	4	US-09-840-009-14
22	54	88.5	18	4	US-09-840-009-20
23	54	88.5	18	4	US-09-840-009-21
24	54	88.5	18	4	US-09-840-009-27
25	54	88.5	18	4	US-09-840-009-28
26	53	86.9	18	4	US-09-840-009-3
27	53	86.9	18	4	US-09-840-009-10

28	53	86.9	18	4	US-09-840-009-17	Sequence 17, Appl
29	53	86.9	18	4	US-09-840-009-24	Sequence 24, Appl
30	53	86.9	18	4	US-09-840-009-31	Sequence 31, Appl
31	53	86.9	18	4	US-09-840-009-34	Sequence 34, Appl
32	53	86.9	18	4	US-09-840-009-35	Sequence 35, Appl
33	45	73.8	18	4	US-09-840-009-32	Sequence 32, Appl
34	45	73.8	18	4	US-09-840-009-33	Sequence 33, Appl
35	45	73.8	18	4	US-09-840-009-36	Sequence 36, Appl
36	45	73.8	18	4	US-09-840-009-37	Sequence 37, Appl
37	41	67.2	18	4	US-09-840-009-1	Sequence 1, Appl
38	39	63.9	391	4	US-09-134-001C-5234	Sequence 5234, Ap
39	38	62.3	24	4	US-09-785-059B-5	Sequence 5, Appl
40	38	62.3	36	4	US-09-785-059B-6	Sequence 6, Appl
41	38	62.3	42	4	US-09-785-059B-7	Sequence 7, Appl
42	38	62.3	48	4	US-09-785-059B-8	Sequence 8, Appl
43	37	60.7	160	4	US-09-917-340-36	Sequence 36, Appl
44	37	60.7	185	4	US-09-902-540-15903	Sequence 15903, A
45	36	59.0	337	4	US-09-538-092-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Maring, Alan J.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT FILING DATE: 2001-04-19
PRIORITY FILING DATE: 2000-06-28
PRIORITY FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match 100.0%; Score 61; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRRIRKIHIIK 13
Db 3 LRRIRKIHIIK 15

RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Maring, Alan J.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT FILING DATE: 2001-04-19
PRIORITY FILING DATE: 2000-06-28
PRIORITY FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 45.5726 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-15
Perfect score: 61
Sequence: 1 LRRIRKIRIK 13

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	13	4	AAB70662
2	61	100.0	14	4	AAB70658
3	61	100.0	14	4	AAB70659
4	61	100.0	14	5	ABP53280
5	61	100.0	14	5	ABP53285
6	61	100.0	16	4	AAB70656
7	61	100.0	16	5	ABP53281
8	61	100.0	18	4	AAB70655
9	61	100.0	18	4	AAB70658
10	61	100.0	18	5	AAE20882
11	61	100.0	18	5	AAE20875
12	61	100.0	18	5	AAE20854
13	61	100.0	18	5	AAE20861
14	61	100.0	18	5	AAE20868
15	61	100.0	18	5	ABP53276
16	61	100.0	18	5	ABP53279
17	61	100.0	29	4	AAB70675
18	61	100.0	29	5	ABP53275
19	59	96.7	14	4	AAB70661
20	59	96.7	14	4	AAB70660
21	59	96.7	14	5	ABP53286
22	59	96.7	14	5	ABP53287
23	59	96.7	16	4	AAB70657
24	59	96.7	16	5	ABP53282
25	59	96.7	18	4	AAB70654

26	59	96.7	18	5	ABP53278	ABP53278 Synthetic
27	59	96.7	18	5	ABP53277	ABP53277 Synthetic
28	59	96.7	20	4	AAB70653	AAB70653 Ovine SMA
29	57	93.4	12	4	AAB70664	AAB70664 Ovine SMA
30	57	93.4	13	4	AAB70663	AAB70663 Ovine SMA
31	56	91.8	18	5	AAE20870	AAE20870 T10-nov1s
32	56	91.8	18	5	AAE20860	AAE20860 D46-nov1s
33	56	91.8	18	5	AAE20881	AAE20881 DA11-nov1
34	56	91.8	18	5	AAE20867	AAE20867 DA10-nov1
35	56	91.8	18	5	AAE20874	AAE20874 DA10-nov1
36	56	91.8	18	5	AAE20863	AAE20863 T7-nov1s
37	56	91.8	18	5	AAE20877	AAE20877 T11-nov1s
38	56	91.8	18	5	AAE20856	AAE20856 T6-nov1s
39	56	91.8	18	5	ABP53292	ABP53292 Synthetic
40	55	90.2	18	5	AAE20864	AAE20864 S7-nov1s
41	55	90.2	18	5	AAE20871	AAE20871 S10-nov1s
42	55	90.2	18	5	AAE20878	AAE20878 S11-nov1s
43	55	90.2	18	5	AAE20857	AAE20857 S6-nov1s
44	54	88.5	18	5	AAE20872	AAE20872 E10-nov1s
45	54	88.5	18	5	AAE20873	AAE20873 D10-nov1s

ALIGNMENTS

RESULT 1
AAB70662
ID AAB70662 standard; peptide; 13 AA.
XX
AC AAB70662;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:15.
XX
KW Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, McCreary P, Welsh M, Travis SM, Lehrer R;
XX
DR WPI; 2001-234911/24.
XX
XX New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
XX Claim 1, Page 103; 137pp; English.
XX
XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (I) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 43.6816 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-14

Perfect score: 66

Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	65.2	638	2	Q8D796
2	43	65.2	660	2	Q7MEAO
3	42	63.6	125	2	Q9AVZ1
4	42	63.6	308	2	Q8R2C7
5	42	63.6	414	2	Q947U2
6	42	63.6	414	2	Q7XEY8
7	42	63.6	500	1	TR3B_SCHPO
8	42	63.6	867	2	Q283J1
9	41	62.1	337	1	YB21_YEAST
10	41	62.1	428	2	Q8TXS5
11	41	62.1	613	1	DEAD_HA2IN
12	41	62.1	670	1	REP_BUCBP
13	41	62.1	1580	2	Q7RMP4
14	41	62.1	2084	2	Q8ILJ6
15	40	60.6	151	2	Q8R891
16	40	60.6	160	1	SC51_SHEEP
17	40	60.6	240	1	SC52_SHEEP
18	40	60.6	240	1	Q7NSJ3
19	40	60.6	256	2	Q83CP2
20	40	60.6	328	2	Q8F1B9
21	40	60.6	328	2	Q8F1B9
22	40	60.6	370	2	Q67743
23	40	60.6	452	2	Q7N787
24	40	60.6	475	2	Q7SGI8
25	40	60.6	671	2	Q8OOU6
26	40	60.6	822	2	Q8ZMW0
27	39	59.1	41	2	Q48971
28	39	59.1	202	1	HAM1_AQUAE
29	39	59.1	210	2	Q92CL5
30	39	59.1	217	2	Q977R2
31	39	59.1	250	2	Q7W5F0

32	39	59.1	250	2	Q7WCYS
33	39	59.1	258	2	Q8MY71
34	39	59.1	295	2	Q13635
35	39	59.1	354	1	H181_OCEIH
36	39	59.1	407	2	Q9UTH1
37	39	59.1	415	2	Q9SPU4
38	39	59.1	460	2	Q9VLO3
39	39	59.1	461	2	Q8IBW2
40	39	59.1	483	2	Q9KRB1
41	39	59.1	549	2	Q8IPC2
42	39	59.1	598	2	Q7VTH0
43	39	59.1	647	2	Q6Z647
44	39	59.1	834	2	Q6FW11
45	39	59.1	866	2	Q8JDU9

ALIGNMENTS

RESULT 1

ID	Q8D796	PRELIMINARY;	PRT;	638 AA.
AC	Q8D796			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Predicted signal transduction protein.			
GN	OrderedLocustNames=VV20264;			
OS	Vibrio vulnificus.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;			
OC	Vibrionaceae; Vibrio.			
OX	NCBI_TaxID=672;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-CMCP6;			
RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,			
RA	Choy H.E.;			
RT	"Complete genome sequence of Vibrio vulnificus CMCP6.";			
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AE016808; AA007230.1; -			
DR	InterPro; IPR001633; EAL.			
DR	InterPro; IPR003018; GAF.			
DR	InterPro; IPR001633; EAL.			
DR	Pfam; PF00563; EAL; 1.			
DR	Pfam; PF01590; GAF; 1.			
DR	Pfam; PF00990; GDEF; 1.			
DR	SMART; SM00052; DUF2; 1.			
DR	SMART; SM00065; GAF; 1.			
DR	TIGRFAMs; TIGR00254; GDEF; 1.			
DR	PROSITE; PS50883; EAL; 1.			
DR	PROSITE; PS50883; GDEF; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64;			

Query Match 65.2%; Score 43; DB 2; Length 638;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 2 RRIIRKIHIIKK 14
566 KEIIRSIHVAKK 578

RESULT 2

ID	Q7MEAO	PRELIMINARY;	PRT;	660 AA.
AC	Q7MEAO			
DT	01-MAR-2004 (TrEMBLrel. 26, Created)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	GGDEF family protein.			
GN	OrderedLocustNames=VVA0770;			
OS	Vibrio vulnificus (strain VJ016).			

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.68156 seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-14

Perfect score: 66

Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	63.6	125	2 A99114	hypothetical prote
2	42	63.6	867	2 G69485	DNA-directed RNA p
3	41	62.1	337	2 S46010	hypothetical prote
4	41	62.1	613	2 P64056	probable ATP-depen
5	40	60.6	152	2 S68411	cathelin-related p
6	40	60.6	160	2 S68412	myeloid antimicrob
7	40	60.6	160	2 S68228	GTP-binding protei
8	39	59.1	41	2 S77768	hypothetical prote
9	39	59.1	202	1 H70318	conserved hypotet
10	39	59.1	210	2 AC1577	precortin isomeras
11	39	59.1	407	2 T37888	hypothetical prote
12	39	59.1	483	2 B82160	hypothetical prote
13	39	59.1	87	2 S00180	spermatid protein
14	38	57.6	234	2 D97108	DNA-dependent RNA
15	38	57.6	234	2 D97108	sigk protein - Cio
16	38	57.6	234	2 D97108	transposase BME114
17	38	57.6	234	2 D97108	transport ATP-bind
18	38	57.6	234	2 D97108	helicase (EC 3.6.1
19	38	57.6	234	2 D97108	2-dehydro-3-deoxy-
20	38	57.6	234	2 D97108	tagatose-bisphosph
21	37	56.1	62	1 R5B53F	hypothetical prote
22	37	56.1	212	2 A64045	ribosomal protein
23	37	56.1	284	2 A10897	2-dehydro-3-deoxy-
24	37	56.1	303	2 P71212	hypothetical prote
25	37	56.1	334	2 B72201	endoglucanase - Th
26	37	56.1	364	2 C70322	3-isopropylmalate
27	37	56.1	368	2 C69984	conserved hypotet
28	37	56.1	483	2 S75369	DNA primase chain
29	37	56.1	569	2 C83952	hypothetical prote

30	37	56.1	813	2 T20527	hypothetical prote
31	37	56.1	856	1 VCLJ3W	env polyprotein pr
32	36	54.5	67	2 B72248	ribosomal protein
33	36	54.5	102	2 AD1420	PTS cellobiose-spe
34	36	54.5	102	2 AE1795	PTS cellobiose-spe
35	36	54.5	117	2 T12722	hypothetical prote
36	36	54.5	299	2 G72307	hypothetical prote
37	36	54.5	310	2 A33489	hypothetical prote
38	36	54.5	370	2 A35034	hypothetical prote
39	36	54.5	447	2 F81678	hypothetical prote
40	36	54.5	499	2 G84972	GTP-binding protei
41	36	54.5	627	2 C82418	leucyl aminopeptid
42	36	54.5	760	2 T24521	GGDEF family prote
43	36	54.5	780	2 AB1801	hypothetical prote
44	36	54.5	849	2 A96592	amino-terminal dom
45	36	54.5	1188	2 C71231	hypothetical prote

ALIGNMENTS

RESULT 1

A99114

hypothetical protein orf125 [imported] - Guillardia theta nucleomorph

C:Species: nucleomorph Guillardia theta

A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004

C:Accession: A99114

R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001

A:Title: The highly reduced genome of an enslaved algal nucleus.

A:Reference number: A99082; MUID:11323671; PMID:11323671

A:Accession: A99114

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-125 <DOU>

A:Cross-references: UNIPROT:Q9AVZ1; GB:AJ010592; NID:gl2580762; PIDN:CAC27080.1; GSPDB:

C:Genetics:

A:Gene: orf125

A:Map position: 2

A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match

Best Local Similarity 63.6%; Score 42; DB 2; Length 125;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IRRIRKIHIIKK 14

DB 9 IRRIRKIHIIKK 18

RESULT 2

G69485

DNA-directed RNA polymerase, subunit A' (rpoA1) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #ext_change 09-Jul-2004

C:Accession: G69485

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso

., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsner, B.F

Nature 390, 364-370, 1997

A:Authors: Uetshack, T.; Cotton, M.D.; Spriggs, T.; Attlich, P.; Kaine, B.P.; Sykes, S

Smith, H.O.; Weese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: G69485

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-867 <KLE>

A:Cross-references: UNIPROT:O28391; GB:AE000972; GB:AE000782; NID:g2689295; PIDN:AA8893

C:Superfamily: Halobacterium DNA-directed RNA polymerase chain A

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds,
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-14
Perfect score: 66
Sequence: 1 IRRIRKIHITIK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	14	14	US-10-060-102-19
2	66	100.0	14	14	US-10-060-102-20
3	66	100.0	14	14	US-10-721-839-19
4	66	100.0	14	14	US-10-721-839-20
5	66	100.0	16	14	US-10-060-102-15
6	66	100.0	16	15	US-10-721-839-15
7	66	100.0	18	14	US-10-060-102-10
8	66	100.0	18	14	US-10-060-102-11
9	66	100.0	18	15	US-10-721-839-10
10	66	100.0	18	15	US-10-721-839-11
11	64	97.0	14	14	US-10-060-102-13
12	64	97.0	14	14	US-10-060-102-18
13	64	97.0	14	15	US-10-721-839-13

14	64	97.0	14	15	US-10-721-839-18	Sequence 18, Appl
15	64	97.0	16	14	US-10-060-102-14	Sequence 14, Appl
16	64	97.0	16	15	US-10-721-839-14	Sequence 14, Appl
17	64	97.0	18	9	US-09-840-009-2	Sequence 2, Appl
18	64	97.0	18	9	US-09-840-009-9	Sequence 9, Appl
19	64	97.0	18	9	US-09-840-009-16	Sequence 16, Appl
20	64	97.0	18	9	US-09-840-009-23	Sequence 23, Appl
21	64	97.0	18	9	US-09-840-009-30	Sequence 30, Appl
22	64	97.0	18	14	US-10-060-102-9	Sequence 9, Appl
23	64	97.0	18	14	US-10-060-102-12	Sequence 12, Appl
24	64	97.0	18	15	US-10-721-839-9	Sequence 9, Appl
25	64	97.0	18	15	US-10-721-839-12	Sequence 12, Appl
26	64	97.0	29	14	US-10-060-102-8	Sequence 8, Appl
27	64	97.0	29	15	US-10-721-839-8	Sequence 8, Appl
28	59	89.4	18	9	US-09-840-009-4	Sequence 4, Appl
29	59	89.4	18	9	US-09-840-009-8	Sequence 8, Appl
30	59	89.4	18	9	US-09-840-009-11	Sequence 11, Appl
31	59	89.4	18	9	US-09-840-009-15	Sequence 15, Appl
32	59	89.4	18	9	US-09-840-009-18	Sequence 18, Appl
33	59	89.4	18	9	US-09-840-009-22	Sequence 22, Appl
34	59	89.4	18	9	US-09-840-009-25	Sequence 25, Appl
35	59	89.4	18	9	US-09-840-009-29	Sequence 29, Appl
36	59	89.4	18	14	US-10-060-102-25	Sequence 25, Appl
37	59	89.4	18	15	US-10-721-839-25	Sequence 25, Appl
38	58	87.9	18	9	US-09-840-009-5	Sequence 5, Appl
39	58	87.9	18	9	US-09-840-009-12	Sequence 12, Appl
40	58	87.9	18	9	US-09-840-009-19	Sequence 19, Appl
41	58	87.9	18	9	US-09-840-009-26	Sequence 26, Appl
42	57	86.4	18	9	US-09-840-009-6	Sequence 6, Appl
43	57	86.4	18	9	US-09-840-009-7	Sequence 7, Appl
44	57	86.4	18	9	US-09-840-009-13	Sequence 13, Appl
45	57	86.4	18	9	US-09-840-009-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-19
; Sequence 19, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STABLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMA
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-10-060-102-19

Query Match 100.0%; Score 66; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IRRIRKIHITIK 14

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744d-14

Perfect score: 66

Sequence: 1 IRRIRKTIHIKK 14

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: Issued Patents AA:
2: /cgn2_6/prodata/1/1aa/5A COMB pep.*
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5: /cgn2_6/prodata/1/1aa/6B COMB pep.*
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8: /cgn2_6/prodata/1/1aa/6E COMB pep.*
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32: /cgn2_6/prodata/1/1aa/6C COMB pep.*
33: /cgn2_6/prodata/1/1aa/6D COMB pep.*
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45: /cgn2_6/prodata/1/1aa/6P COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	18	4	US-09-840-009-2
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4	64	97.0	18	4	US-09-840-009-23
5	64	97.0	18	4	US-09-840-009-30
6	59	89.4	18	4	US-09-840-009-4
7	59	89.4	18	4	US-09-840-009-8
8	59	89.4	18	4	US-09-840-009-11
9	59	89.4	18	4	US-09-840-009-15
10	59	89.4	18	4	US-09-840-009-18
11	59	89.4	18	4	US-09-840-009-22
12	59	89.4	18	4	US-09-840-009-25
13	59	89.4	18	4	US-09-840-009-29
14	58	87.9	18	4	US-09-840-009-12
15	58	87.9	18	4	US-09-840-009-19
16	58	87.9	18	4	US-09-840-009-26
17	58	87.9	18	4	US-09-840-009-3
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19	57	86.4	18	4	US-09-840-009-7
20	57	86.4	18	4	US-09-840-009-13
21	57	86.4	18	4	US-09-840-009-14
22	57	86.4	18	4	US-09-840-009-20
23	57	86.4	18	4	US-09-840-009-21
24	57	86.4	18	4	US-09-840-009-27
25	57	86.4	18	4	US-09-840-009-28
26	56	84.8	18	4	US-09-840-009-3
27	56	84.8	18	4	US-09-840-009-10

28	56	84.8	18	4	US-09-840-009-17	Sequence 17, Appl
29	56	84.8	18	4	US-09-840-009-24	Sequence 24, Appl
30	56	84.8	18	4	US-09-840-009-31	Sequence 31, Appl
31	56	84.8	18	4	US-09-840-009-34	Sequence 34, Appl
32	56	84.8	18	4	US-09-840-009-35	Sequence 35, Appl
33	48	72.7	18	4	US-09-840-009-32	Sequence 32, Appl
34	48	72.7	18	4	US-09-840-009-33	Sequence 33, Appl
35	48	72.7	18	4	US-09-840-009-36	Sequence 36, Appl
36	48	72.7	18	4	US-09-840-009-37	Sequence 37, Appl
37	44	66.7	18	4	US-09-840-009-1	Sequence 1, Appl
38	42	63.6	24	4	US-09-785-0598-5	Sequence 5, Appl
39	42	63.6	36	4	US-09-785-0598-6	Sequence 6, Appl
40	42	63.6	42	4	US-09-785-0598-7	Sequence 7, Appl
41	42	63.6	48	4	US-09-785-0598-8	Sequence 8, Appl
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43	41	62.1	391	3	US-09-134-001C-5234	Sequence 5234, Ap
44	40	60.6	160	4	US-09-917-340-36	Sequence 36, Appl
45	40	60.6	169	4	US-09-917-340-36	Sequence 35406, A

ALIGNMENTS

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RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lebrer, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          97.0%   Score 64;   DB 4;   Length 18;
Best Local Similarity 92.9%   Pred. No. 0.00098;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 IRRIRKTIHIKK 14
DB      3 LRRIRKTIHIKK 16
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lebrer, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-14

Sequence: 1 IRRIRKIHIIKK 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: geneseqp20038.*
7: geneseqp20048.*
8: geneseqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	14	4	AAB70661
2	66	100.0	14	4	AAB70660
3	66	100.0	14	5	ABP53286
4	66	100.0	14	5	ABP53287
5	66	100.0	16	4	AAB70657
6	66	100.0	16	5	ABP53282
7	66	100.0	18	4	AAB70654
8	66	100.0	18	5	ABP53278
9	66	100.0	18	5	ABP53277
10	66	100.0	20	4	AAB70653
11	66	97.0	14	4	AAB70658
12	64	97.0	14	4	AAB70659
13	64	97.0	14	5	ABP53280
14	64	97.0	14	5	ABP53285
15	64	97.0	16	4	AAB70656
16	64	97.0	16	5	ABP53281
17	64	97.0	18	4	AAB70655
18	64	97.0	18	4	AAB70648
19	64	97.0	18	5	ABP53282
20	64	97.0	18	5	ABP53281
21	64	97.0	18	5	ABP53285
22	64	97.0	18	5	ABP53286
23	64	97.0	18	5	ABP53287
24	64	97.0	18	5	ABP53288
25	64	97.0	18	5	ABP53289

25	64	97.0	29	4	AAB70675	AAB70675
27	64	97.0	29	5	ABP53275	ABP53275
28	62	93.9	13	4	AAB70663	AAB70663
29	59	89.4	13	4	AAB70662	AAB70662
30	59	89.4	18	5	AAB70670	AAB70670
31	59	89.4	18	5	AAB70680	AAB70680
32	59	89.4	18	5	AAB70681	AAB70681
33	59	89.4	18	5	AAB70687	AAB70687
34	59	89.4	18	5	AAB70684	AAB70684
35	59	89.4	18	5	AAB70683	AAB70683
36	59	89.4	18	5	AAB70687	AAB70687
37	59	89.4	18	5	AAB70686	AAB70686
38	59	89.4	18	5	AAB70685	AAB70685
39	58	87.9	18	5	AAB70684	AAB70684
40	58	87.9	18	5	AAB70687	AAB70687
41	58	87.9	18	5	AAB70687	AAB70687
42	58	87.9	18	5	AAB70687	AAB70687
43	57	86.4	12	4	AAB70664	AAB70664
44	57	86.4	18	5	AAB70687	AAB70687
45	57	86.4	18	5	AAB70687	AAB70687

ALIGNMENTS

RESULT 1	AAB70661	standard; peptide; 14 AA.
ID	AAB70661	standard; peptide; 14 AA.
XX	AC	AAB70661;
XX	DT	15-MAY-2001 (first entry)
XX	DE	Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:14.
XX	DE	Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:14.
XX	KW	Ovine: SNAP29; lupine: RCAP 18; cathelicidin; antimicrobial;
XX	KW	bactericidal; antibiotic; antiviral; microbial growth inhibitor;
XX	KW	proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX	KW	Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX	OS	Ovis aries.
XX	PN	MO200112668-A1.
XX	PD	22-FEB-2001.
XX	PF	18-AUG-2000; 2000MO-US022781.
XX	PR	18-AUG-1999; 99US-0149886P.
XX	PA	(IOWA) UNIV IOWA RES FOUND.
XX	PA	(REGC) UNIV CALIFORNIA.
XX	PI	Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX	DR	WPI; 2001-234911/24.
XX	PT	New antimicrobial peptides useful as antibiotics for inhibiting growth
XX	PT	and proliferation of microbes, and for treating microbial infections.
XX	PS	Claim 1; Page 103; 137p; English.
XX	CC	AAB70648 to AAB70675 represent antimicrobial peptides (1), of which
XX	CC	AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX	CC	SNAP 29 cathelicidin family peptide, and AAB70673 are derived
XX	CC	from the lupine RCAP 18 cathelicidin family peptide. (1) have antibiotic,
XX	CC	antimicrobial and antiviral activities, and can be used as microbial
XX	CC	growth and proliferation inhibitors and in gene therapy (1) are useful
XX	CC	for inhibiting microbial growth in an environment capable of sustaining
XX	CC	such growth, for inhibiting microbial growth or strain in a host, and
XX	CC	inhibiting the growth of drug-resistant microbial strains such as
XX	CC	Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 43.6816 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-13

Perfect score: 66

Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	65.2	638	2 Q8D796	Q8D796 vibrio vuln
2	43	65.2	660	2 Q7MEAO	Q7MEAO vibrio vuln
3	42	63.6	125	2 Q9AVZ1	Q9AVZ1 guillardi
4	42	63.6	308	2 Q8R2C7	Q8R2C7 mus musculi
5	42	63.6	414	2 Q94702	Q94702 oryza sativ
6	42	63.6	414	2 Q7XEY8	Q7XEY8 oryza sativ
7	42	63.6	500	1 TF3B_SCHPO	TF3B_SCHPO
8	42	63.6	867	2 Q28391	Q28391 schizosach
9	41	62.1	337	1 YBZ1_YEAST	YBZ1_YEAST
10	41	62.1	428	2 Q8TXS5	Q8TXS5 methanopyru
11	41	62.1	613	1 DEAD_HAEIN	DEAD_HAEIN
12	41	62.1	670	1 REP_BUCBP	REP_BUCBP
13	41	62.1	1580	2 Q7RMP4	Q7RMP4 plasmodium
14	41	62.1	2084	2 Q8ILJ6	Q8ILJ6 plasmodium
15	40	60.6	151	2 Q8R891	Q8R891 thermotac
16	40	60.6	160	1 SC51_SHEEP	SC51_SHEEP
17	40	60.6	160	1 SC51_SHEEP	SC51_SHEEP
18	40	60.6	240	2 Q7NSJ3	Q7NSJ3 ovis aries
19	40	60.6	256	2 Q83CP2	Q83CP2 coxiella bu
20	40	60.6	328	2 Q72TV1	Q72TV1 leptospira
21	40	60.6	328	2 Q8F1B9	Q8F1B9 leptospira
22	40	60.6	370	2 Q67743	Q67743 aquilex aeo
23	40	60.6	452	2 Q7N787	Q7N787 photorhabd
24	40	60.6	475	2 Q7S6I8	Q7S6I8 oryza sativ
25	40	60.6	822	2 Q8Q0U6	Q8Q0U6 methanosarc
26	39	59.1	41	2 Q48971	Q48971 pyrobaculum
27	39	59.1	202	1 HANI_AQUAE	HANI_AQUAE
28	39	59.1	210	2 Q92C15	Q92C15 mycoplasma
29	39	59.1	217	2 Q977R2	Q977R2 aquilex aeo
30	39	59.1	217	2 Q977R2	Q977R2 listeria in
31	39	59.1	250	2 Q7W5F0	Q7W5F0 uncultured
					Q7W5F0 bordetella

32	39	59.1	250	2 Q7WCY5	Q7WCY5 bordetella
33	39	59.1	258	2 Q8MY71	Q8MY71 brachionus
34	39	59.1	295	2 Q13635	Q13635 schizosach
35	39	59.1	354	1 H1B1_OCEIH	H1B1_OCEIH
36	39	59.1	407	2 Q9UTH1	Q9UTH1 oceanobacil
37	39	59.1	415	2 Q9SPU4	Q9SPU4 schizosach
38	39	59.1	460	2 Q9V1O3	Q9V1O3 nicotiana t
39	39	59.1	461	2 Q8IBW2	Q8IBW2 dirosophila
40	39	59.1	483	2 Q9XR81	Q9XR81 plasmodium
41	39	59.1	549	2 Q8IPC2	Q8IPC2 vibrio chol
42	39	59.1	598	2 Q7VTH0	Q7VTH0 dirosophila
43	39	59.1	647	2 Q6Z647	Q6Z647 bordetella
44	39	59.1	834	2 Q6FW11	Q6FW11 oryza sativ
45	39	59.1	866	2 Q8JDJ9	Q8JDJ9 candida gla
					Q8JDJ9 human immun

ALIGNMENTS

RESULT 1					
ID	Q8D796	PRELIMINARY;	PRT;	638 AA.	
AC	Q8D796;				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Predicted signal transduction protein.				
GN	OrderedLocustNames=VV20264;				
OS	Vibrio vulnificus.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;				
OC	Vibrionaceae; Vibrio.				
OX	NCBI_TaxID=672;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SRATIN=CMCP6;				
RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,				
RA	Choy H.B.;				
RT	"Complete genome sequence of Vibrio vulnificus CMCP6.";				
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AE016808; AA007230.1; -				
DR	InterPro; IPR001633; EAL.				
DR	InterPro; IPR003018; GAF.				
DR	InterPro; IPR000160; GDEF.				
DR	Pfam; PF00563; EAL; 1.				
DR	Pfam; PF01590; GAF; 1.				
DR	Pfam; PF00990; GDEF; 1.				
DR	SMART; SM00052; DUF2; 1.				
DR	SMART; SM00065; GAF; 1.				
DR	TIGRFAMs; TIGR00254; GDEF; 1.				
DR	PROSITE; PS00883; EAL; 1.				
DR	PROSITE; PS00887; GDEF; 1.				
KW	Complete proteome.				
SO	SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64;				
Query Match					
Best Local Similarity 65.2%; Score 43; DB 2; Length 638;					
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;					
Qy	2 RRIIRKIHIIKK 14				
Db	566 KEIRSIHIVAKK 578				
RESULT 2					
ID	Q7MEAO	PRELIMINARY;	PRT;	660 AA.	
AC	Q7MEAO;				
DT	01-MAR-2004 (TREMBLrel. 26, Created)				
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)				
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	GDEF family protein.				
GN	OrderedLocustNames=VVA0770;				
OS	Vibrio vulnificus (strain VJ016).				

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.68156 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-13

Perfect score: 66

Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	63.6	125	2 A99114	hypothetical prote
2	42	63.6	867	2 G69485	DNA-directed RNA p
3	41	62.1	337	2 S46010	hypothetical prote
4	41	62.1	613	2 F64056	probable ATP-depen
5	40	60.6	152	2 S68411	catheлин-related p
6	40	60.6	160	2 S68412	myeloid antimicrob
7	40	60.6	160	2 S68228	GTP-binding protei
8	40	60.6	370	2 C70464	hypothetical prote
9	39	59.1	41	2 S77768	conserved hypotet
10	39	59.1	202	1 H70318	precortin isomeras
11	39	59.1	210	2 AC1577	hypothetical prote
12	39	59.1	407	2 T37888	hypothetical prote
13	39	59.1	483	2 B82160	spermatid protein
14	38	57.6	87	2 S00180	DNA-dependent RNA
15	38	57.6	234	2 D97108	sigk protein - Clo
16	38	57.6	222	2 AB3430	transposase BME114
17	38	57.6	623	2 S73436	transposase ATP-bind
18	38	57.6	623	2 D64084	heiliase (BC 3.6.1
19	38	57.6	62	1 R5B53F	ribosomal protein
20	37	56.1	212	2 A64045	2-dehydro-3-deoxy-
21	37	56.1	284	2 A10897	tagarose-bisphosph
22	37	56.1	303	2 F71212	hypothetical prote
23	37	56.1	334	2 B72301	endooglucanase - Th
24	37	56.1	364	2 C70322	3-isopropylmalate
25	37	56.1	368	2 C69984	conserved hypotet
26	37	56.1	420	2 S45630	DNA primase chain
27	37	56.1	483	2 S75369	hypothetical prote
28	37	56.1	569	2 C83952	prolyl-tRNA synth

30	37	56.1	813	2 T20527	hypothetical prote
31	37	56.1	856	1 VCLJ3W	env polyprotein pr
32	36	54.5	67	2 B72248	ribosomal protein
33	36	54.5	102	2 AD1420	PTS cellobiose-spe
34	36	54.5	102	2 AE1795	PTS cellobiose-spe
35	36	54.5	117	2 T12722	hypothetical prote
36	36	54.5	299	2 G72307	hypothetical prote
37	36	54.5	310	2 A33489	hypothetical prote
38	36	54.5	370	2 A05034	hypothetical prote
39	36	54.5	447	2 F81678	GTP-binding protei
40	36	54.5	499	2 G84972	leucyl aminopeptid
41	36	54.5	627	2 C82418	GDEF family prote
42	36	54.5	760	2 T24521	hypothetical prote
43	36	54.5	780	2 AB1801	amino-terminal dom
44	36	54.5	849	2 A96592	hypothetical prote
45	36	54.5	1188	2 C71231	hypothetical prote

ALIGNMENTS

RESULT 1

A99114 hypothetical protein orf125 [imported] - Guillardia theta nucleomorph

C/Species: nucleomorph Guillardia theta

C/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: A99114

R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001

A/Title: The highly reduced genome of an enslaved algal nucleus.

A/Reference number: A99082; WUID:11323671; PMID:11323671

A/Accession: A99114

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-125 <DOU>

A/Cross-references: UNIPROT:Q9AVZ1; GB:AJ010592; NID:G12580762; PIDN:CAC27080.1; GSPDB:

A/Genetic: A/Genetic:

A/Map position: 2

A/Genome: nucleomorph

C/Keywords: nucleomorph

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Score 42; DB 2; Length 125;

70.0%; Pred. No. 6.6;

3; Mismatches 0; Indels 0; Gaps 0;

0; Indels 0; Gaps 0;

30	37	56.1	813	2 T20527	hypothetical prote
31	37	56.1	856	1 VCLJ3W	env polyprotein pr
32	36	54.5	67	2 B72248	ribosomal protein
33	36	54.5	102	2 AD1420	PTS cellobiose-spe
34	36	54.5	102	2 AE1795	PTS cellobiose-spe
35	36	54.5	117	2 T12722	hypothetical prote
36	36	54.5	299	2 G72307	hypothetical prote
37	36	54.5	310	2 A33489	hypothetical prote
38	36	54.5	370	2 A05034	hypothetical prote
39	36	54.5	447	2 F81678	GTP-binding protei
40	36	54.5	499	2 G84972	leucyl aminopeptid
41	36	54.5	627	2 C82418	GDEF family prote
42	36	54.5	760	2 T24521	hypothetical prote
43	36	54.5	780	2 AB1801	amino-terminal dom
44	36	54.5	849	2 A96592	hypothetical prote
45	36	54.5	1188	2 C71231	hypothetical prote

RESULT 2
G69485 DNA-directed RNA polymerase, subunit A' (rpoA1) homolog - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: G69485
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodac
., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirtness, E.;
Nature 390, 364-370, 1997
A/Authors: Uetzelbeck, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kahne, B.P.; Sykes, S
Smith, H.O.; Moese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A/Reference number: A69250; WUID:98049343; PMID:9389475
A/Accession: G69485
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-867 <KLE>
A/Cross-references: UNIPROT:028391; GB:AB000972; GB:AB000782; NID:G2689295; PIDN:AA8893
C/Superfamily: Halobacterium DNA-directed RNA polymerase chain A

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OM protein - protein search, using SW model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-13

Perfect score: 66

Sequence: 1 IRRIRKIHITIKK 14

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 33106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	14	US-10-060-102-19	Sequence 19, Appl
2	66	100.0	14	US-10-060-102-20	Sequence 20, Appl
3	66	100.0	14	US-10-721-839-19	Sequence 19, Appl
4	66	100.0	14	US-10-721-839-20	Sequence 20, Appl
5	66	100.0	16	US-10-060-102-15	Sequence 15, Appl
6	66	100.0	16	US-10-721-839-15	Sequence 15, Appl
7	66	100.0	18	US-10-060-102-10	Sequence 10, Appl
8	66	100.0	18	US-10-060-102-11	Sequence 11, Appl
9	66	100.0	18	US-10-721-839-10	Sequence 10, Appl
10	66	100.0	18	US-10-721-839-11	Sequence 11, Appl
11	64	97.0	14	US-10-060-102-13	Sequence 13, Appl
12	64	97.0	14	US-10-060-102-16	Sequence 16, Appl
13	64	97.0	14	US-10-721-839-13	Sequence 13, Appl

14	64	97.0	14	US-10-721-839-18	Sequence 18, Appl
15	64	97.0	16	US-10-060-102-14	Sequence 14, Appl
16	64	97.0	16	US-10-721-839-14	Sequence 14, Appl
17	64	97.0	18	US-09-840-009-2	Sequence 2, Appl
18	64	97.0	9	US-09-840-009-9	Sequence 9, Appl
19	64	97.0	18	US-09-840-009-16	Sequence 16, Appl
20	64	97.0	18	US-09-840-009-23	Sequence 23, Appl
21	64	97.0	18	US-09-840-009-30	Sequence 30, Appl
22	64	97.0	18	US-10-060-102-9	Sequence 9, Appl
23	64	97.0	18	US-10-060-102-12	Sequence 12, Appl
24	64	97.0	18	US-10-721-839-9	Sequence 9, Appl
25	64	97.0	18	US-10-721-839-12	Sequence 12, Appl
26	64	97.0	29	US-10-060-102-8	Sequence 8, Appl
27	64	97.0	29	US-10-721-839-8	Sequence 8, Appl
28	59	89.4	18	US-09-840-009-4	Sequence 4, Appl
29	59	89.4	18	US-09-840-009-8	Sequence 8, Appl
30	59	89.4	18	US-09-840-009-11	Sequence 11, Appl
31	59	89.4	18	US-09-840-009-15	Sequence 15, Appl
32	59	89.4	18	US-09-840-009-18	Sequence 18, Appl
33	59	89.4	18	US-09-840-009-22	Sequence 22, Appl
34	59	89.4	18	US-09-840-009-25	Sequence 25, Appl
35	59	89.4	18	US-09-840-009-29	Sequence 29, Appl
36	59	89.4	18	US-10-060-102-25	Sequence 25, Appl
37	59	89.4	18	US-10-721-839-25	Sequence 25, Appl
38	58	87.9	18	US-09-840-009-5	Sequence 5, Appl
39	58	87.9	18	US-09-840-009-12	Sequence 12, Appl
40	58	87.9	18	US-09-840-009-19	Sequence 19, Appl
41	58	87.9	18	US-09-840-009-26	Sequence 26, Appl
42	57	86.4	18	US-09-840-009-7	Sequence 7, Appl
43	57	86.4	18	US-09-840-009-13	Sequence 13, Appl
44	57	86.4	18	US-09-840-009-13	Sequence 13, Appl
45	57	86.4	9	US-09-840-009-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-19
Sequence 19, Application US/10060102
Publication No. US2003022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINKS, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA.035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-19

Query Match 100.0%; Score 66; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IRRIRKIHITIKK 14

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-13
Perfect score: 66
Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCFUS COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfUS1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	97.0	18	4	US-09-840-009-2
2	64	97.0	18	4	US-09-840-009-9
3	64	97.0	18	4	US-09-840-009-16
4	64	97.0	18	4	US-09-840-009-23
5	64	97.0	18	4	US-09-840-009-30
6	59	89.4	18	4	US-09-840-009-4
7	59	89.4	18	4	US-09-840-009-8
8	59	89.4	18	4	US-09-840-009-11
9	59	89.4	18	4	US-09-840-009-15
10	59	89.4	18	4	US-09-840-009-18
11	59	89.4	18	4	US-09-840-009-22
12	59	89.4	18	4	US-09-840-009-25
13	59	89.4	18	4	US-09-840-009-29
14	58	87.9	18	4	US-09-840-009-5
15	58	87.9	18	4	US-09-840-009-12
16	58	87.9	18	4	US-09-840-009-19
17	58	87.9	18	4	US-09-840-009-26
18	57	86.4	18	4	US-09-840-009-6
19	57	86.4	18	4	US-09-840-009-7
20	57	86.4	18	4	US-09-840-009-13
21	57	86.4	18	4	US-09-840-009-14
22	57	86.4	18	4	US-09-840-009-20
23	57	86.4	18	4	US-09-840-009-21
24	57	86.4	18	4	US-09-840-009-27
25	57	86.4	18	4	US-09-840-009-28
26	56	84.8	18	4	US-09-840-009-3
27	56	84.8	18	4	US-09-840-009-10

28	56	84.8	18	4	US-09-840-009-17	Sequence 17, Appl
29	56	84.8	18	4	US-09-840-009-24	Sequence 24, Appl
30	56	84.8	18	4	US-09-840-009-31	Sequence 31, Appl
31	56	84.8	18	4	US-09-840-009-34	Sequence 34, Appl
32	56	84.8	18	4	US-09-840-009-35	Sequence 35, Appl
33	48	72.7	18	4	US-09-840-009-32	Sequence 32, Appl
34	48	72.7	18	4	US-09-840-009-33	Sequence 33, Appl
35	48	72.7	18	4	US-09-840-009-36	Sequence 36, Appl
36	48	72.7	18	4	US-09-840-009-37	Sequence 37, Appl
37	44	66.7	18	4	US-09-840-009-1	Sequence 1, Appl
38	42	63.6	24	4	US-09-785-0598-5	Sequence 5, Appl
39	42	63.6	36	4	US-09-785-0598-6	Sequence 6, Appl
40	42	63.6	42	4	US-09-785-0598-7	Sequence 7, Appl
41	42	62.1	48	4	US-09-785-0598-8	Sequence 8, Appl
42	41	62.1	337	4	US-09-538-092-38	Sequence 38, Appl
43	41	62.1	391	3	US-09-134-001C-5234	Sequence 5234, Ap
44	40	60.6	160	4	US-09-917-340-35	Sequence 35, Appl
45	40	60.6	169	4	US-09-270-767-35406	Sequence 35406, A

ALIGNMENTS

```

RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
  
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Query Match          97.0%; Score 64; DB 4; Length 18;
Best Local Similarity 92.9%; Pred. No. 0.00098;
Matches 13; Conservative 1; Mismatches 0; Indels 0;
  
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QY 1 IRRIRKIHIIKK 14

DB 3 LRRIRKIHIIKK 16

US-09-840-009-9

Sequence 9, Application US/09840009

Patent No. 6492328

GENERAL INFORMATION:

APPLICANT: Lehner, Robert I.

APPLICANT: Waring, Alan J.

APPLICANT: Tack, Brian F.

TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES

FILE REFERENCE: 06510-195WO

CURRENT APPLICATION NUMBER: US/09/840,009

PRIOR FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds

(without alignment)
110.327 Million cell updates/sec

Title: US-09-642-744D-13

Perfect score: 66

Sequence: 1 IRRIRKIRIRIKK 14

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	14	4 AAB70661	Aab70661 Ovine SMA
2	66	100.0	14	4 AAB70660	Aab70660 Ovine SMA
3	66	100.0	14	5 ABP53286	ABP53286 Synthetic
4	66	100.0	14	5 ABP53287	ABP53287 Synthetic
5	66	100.0	16	4 AAB70657	Aab70657 Ovine SMA
6	66	100.0	16	5 ABP53282	ABP53282 Synthetic
7	66	100.0	18	4 AAB70654	Aab70654 Ovine SMA
8	66	100.0	18	5 ABP53278	ABP53278 Synthetic
9	66	100.0	18	5 ABP53277	ABP53277 Synthetic
10	66	100.0	20	4 AAB70653	Aab70653 Ovine SMA
11	64	97.0	14	4 AAB70658	Aab70658 Ovine SMA
12	64	97.0	14	4 AAB70659	Aab70659 Ovine SMA
13	64	97.0	14	5 ABP53280	ABP53280 Synthetic
14	64	97.0	14	5 ABP53285	ABP53285 Synthetic
15	64	97.0	16	4 AAB70656	Aab70656 Ovine SMA
16	64	97.0	18	5 ABP53281	ABP53281 Synthetic
17	64	97.0	18	4 AAB70655	Aab70655 Ovine SMA
18	64	97.0	18	4 AAB70648	Aab70648 Ovine SMA
19	64	97.0	18	5 AAE20882	AAE20882 D11-nov1
20	64	97.0	18	5 AAE20875	AAE20875 D11-nov1
21	64	97.0	18	5 AAE20854	AAE20854 Ovispirin
22	64	97.0	18	5 AAE20861	AAE20861 D16-nov1
23	64	97.0	18	5 AAE20868	AAE20868 D17-nov1
24	64	97.0	18	5 ABP53276	ABP53276 Synthetic
25	64	97.0	18	5 ABP53279	ABP53279 Synthetic

26	64	97.0	29	4 AAB70675	Aab70675 Ovine SMA
27	64	97.0	29	5 ABP53275	ABP53275 Synthetic
28	62	93.9	13	4 AAB70663	Aab70663 Ovine SMA
29	59	89.4	13	4 AAB70662	Aab70662 Ovine SMA
30	59	89.4	18	5 AAE20870	AAE20870 T10-nov1
31	59	89.4	18	5 AAE20860	AAE20860 DAE-nov1
32	59	89.4	18	5 AAE20881	AAE20881 DAI1-nov1
33	59	89.4	18	5 AAE20867	AAE20867 DAI1-nov1
34	59	89.4	18	5 AAE20874	AAE20874 DAI0-nov1
35	59	89.4	18	5 AAE20863	AAE20863 T7-nov1
36	59	89.4	18	5 AAE20877	AAE20877 T11-nov1
37	59	89.4	18	5 AAE20856	AAE20856 T6-nov1
38	59	89.4	18	5 ABP53292	ABP53292 Synthetic
39	58	87.9	18	5 AAE20864	AAE20864 S7-nov1
40	58	87.9	18	5 AAE20871	AAE20871 S10-nov1
41	58	87.9	18	5 AAE20878	AAE20878 S11-nov1
42	58	87.9	18	5 AAE20857	AAE20857 S6-nov1
43	57	86.4	12	4 AAB70664	Aab70664 Ovine SMA
44	57	86.4	18	5 AAE20872	AAE20872 E10-nov1
45	57	86.4	18	5 AAE20873	AAE20873 D10-nov1

ALIGNMENTS

RESULT 1	
AAB70661	
ID AAB70661 standard; peptide; 14 AA.	
XX	
AC AAB70661;	
XX	
DT 15-MAY-2001 (first entry)	
XX	
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:14.	
XX	
KM Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;	
KM bactericidal; antibiotic; antiviral; microbial growth inhibitor;	
KM proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;	
KM Burkholderia cepacia; Alcaligenes; Xanthomonas.	
XX	
OS Ovis aries.	
XX	
PN WO200112668-A1.	
XX	
PD 22-FEB-2001.	
XX	
PF 18-AUG-2000; 2000MO-US022781.	
XX	
PR 18-AUG-1999; 99US-0149886P.	
XX	
PA (IOWA) UNIV IOWA RES FOUND.	
PA (REGC) UNIV CALIFORNIA.	
XX	
PI Tick BE, Mccray P, Welsh M, Travis SM, Lehrer R,	
XX	
DR WPI; 2001-234911/24.	
XX	
PT New antimicrobial peptides useful as antibiotics for inhibiting growth	
PT and proliferation of microbes, and for treating microbial infections.	
XX	
PS Claim 1; Page 103; 137pp; English.	
XX	
CC AAB70648 to AAB70675 represent antimicrobial peptides (I), of which	
CC SNAP 29 cathelicidin family peptide, and AAB70675 are derived from the ovine	
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine	
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,	
CC antimicrobial and antiviral activities, and can be used as microbial	
CC growth and proliferation inhibitors and in gene therapy. (II) are useful	
CC for inhibiting microbial growth in an environment capable of sustaining	
CC such growth, for inhibiting microbial growth or strain in a host, and	
CC inhibiting the growth of drug-resistant microbial strains such as	
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas	
XX	

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 / Search time 43.6816 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-12

Sequence: 1 LRRIKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	65.2	638	2	Q8D796
2	43	65.2	660	2	Q7MEAO
3	42	63.6	125	2	Q9AVZ1
4	42	63.6	160	1	SCS1_SHEEP
5	42	63.6	160	1	SCS2_SHEEP
6	42	63.6	308	2	Q8R2C7
7	42	63.6	500	1	TF3B_SCHRO
8	41	62.1	41	2	Q48971
9	41	62.1	217	2	Q977R2
10	41	62.1	337	1	YBZ1_YEAST
11	41	62.1	414	2	Q7XEV8
12	41	62.1	613	2	Q7XEV8
13	41	62.1	613	1	DEAD_HAEN
14	41	62.1	670	1	RBP_BUCBP
15	40	60.6	256	2	Q85CP2
16	40	60.6	370	2	Q67743
17	40	60.6	452	2	Q7N787
18	40	60.6	461	2	Q81BM2
19	40	60.6	475	2	Q75G18
20	40	60.6	867	2	Q28391
21	39	59.1	202	1	HAML_AQUAE
22	39	59.1	210	2	Q92CL5
23	39	59.1	250	2	Q7W5F0
24	39	59.1	250	2	Q7W5F0
25	39	59.1	258	2	Q8MY71
26	39	59.1	349	2	Q736D5
27	39	59.1	349	2	Q81P89
28	39	59.1	349	2	Q6H112
29	39	59.1	407	2	Q9UTM1
30	39	59.1	428	2	Q8TXS5
31	39	59.1	483	2	Q9KR81

32	39	59.1	598	2	Q7VTH0	Q7VTH0
33	39	59.1	838	2	Q9DVL4	Q9DVL4
34	39	59.1	903	2	Q95WA7	Q95WA7
35	39	59.1	967	2	Q7RJB4	Q7RJB4
36	39	59.1	1157	2	Q7RONS	Q7RONS
37	39	59.1	1160	2	Q7SBL3	Q7SBL3
38	39	59.1	1226	2	Q6L573	Q6L573
39	39	59.1	1580	2	Q7RMP4	Q7RMP4
40	39	59.1	2084	2	Q81J6	Q81J6
41	39	59.1	4057	2	Q81J6	Q81J6
42	38	57.6	87	1	SSS1_SCYCA	SSS1_SCYCA
43	38	57.6	102	2	Q8Y3R8	Q8Y3R8
44	38	57.6	102	2	Q926Y2	Q926Y2
45	38	57.6	102	2	Q71VZ6	Q71VZ6

ALIGNMENTS

RESULT 1

ID Q8D796 PRELIMINARY; PRT; 638 AA.

AC Q8D796; 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DE Predicted signal transduction protein.

OS OrderedLocustNames=V20264;

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrrio.

OX NCBI_TaxID=672;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CMCP6;

RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

RA Choy H.E.;

RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AEO16808; AAC07230.1; -

DR InterPro; IPR001633; EAL.

DR InterPro; IPR003018; GAF.

DR InterPro; IPR00160; GDEF.

DR Pfam; PF00563; EAL; 1.

DR Pfam; PF01590; GAF; 1.

DR Pfam; PF00990; GDEF; 1.

DR SMART; SM00052; DUF2; 1.

DR SMART; SM00065; GAF; 1.

DR TIGRFAMs; TIGR00254; GDEF; 1.

DR PROSITE; PSS0883; EAL; 1.

DR PROSITE; PSS0887; GDEF; 1.

KW Complete proteome.

SO SEQUENCE 638 AA; 72187 MW; 7D13E2BDF3A3F099 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 638;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LRRIKIHIIKK 14
Db 566 KEIRIRIHVAKK 578

RESULT 2

ID Q7MEAO PRELIMINARY; PRT; 660 AA.

AC Q7MEAO; 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DE Predicted signal transduction protein.

OS OrderedLocustNames=VVA0770;

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrrio.

OX NCBI_TaxID=672;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CMCP6;

RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

RA Choy H.E.;

RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AEO16808; AAC07230.1; -

DR InterPro; IPR001633; EAL.

DR InterPro; IPR003018; GAF.

DR InterPro; IPR00160; GDEF.

DR Pfam; PF00563; EAL; 1.

DR Pfam; PF01590; GAF; 1.

DR Pfam; PF00990; GDEF; 1.

DR SMART; SM00052; DUF2; 1.

DR SMART; SM00065; GAF; 1.

DR TIGRFAMs; TIGR00254; GDEF; 1.

DR PROSITE; PSS0883; EAL; 1.

DR PROSITE; PSS0887; GDEF; 1.

KW Complete proteome.

SO SEQUENCE 638 AA; 72187 MW; 7D13E2BDF3A3F099 CRC64;

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.68156 Seconds
(without alignment)
155.160 Million cell updates/sec

Title: US-09-642-744D-12
Sequence: 1 LRRIKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	63.6	125	2 A99114	hypothetical prote
2	42	63.6	152	2 S68411	cathelin-related p
3	42	63.6	160	2 S68412	cathelin-related p
4	42	63.6	160	2 S68228	myeloid antimicrob
5	41	62.1	41	2 S77768	hypothetical prote
6	41	62.1	337	2 S46010	hypothetical prote
7	41	62.1	613	2 F64056	probable ATP-depen
8	40	60.6	370	2 C70464	GTP-binding protei
9	40	60.6	867	2 G69485	DNA-directed RNA p
10	39	59.1	202	1 H70318	conserved hypothet
11	39	59.1	210	2 AC1577	precocarin isomeras
12	39	59.1	407	2 T17888	hypothetical prote
13	39	59.1	483	2 B82160	hypothetical prote
14	38	57.6	87	2 S00180	spermatid protein
15	38	57.6	102	2 AD1420	hypothetical prote
16	38	57.6	102	2 AB1795	PTS cellobiose-spe
17	38	57.6	272	2 AB3430	transposase BME14
18	38	57.6	284	2 A10897	transposase-bisphosph
19	38	57.6	623	2 S73462	transport ATP-bind
20	38	57.6	698	2 D64084	helicase (EC 3.6.1
21	38	57.6	780	2 AB1801	amino-terminal dom
22	38	57.6	1188	2 C71231	hypothetical prote
23	37	56.1	334	2 B72301	endoglucanase - Th
24	37	56.1	352	2 H86454	CDS protein P9L1.
25	37	56.1	352	2 H86454	conserved hypothet
26	37	56.1	352	2 H86454	prolyl-tRNA synthet
27	37	56.1	352	2 H86454	alanine-tRNA ligase
28	36	54.5	117	2 T12722	hypothetical prote
29	36	54.5	234	2 D97108	DNA-dependent RNA

30	36	54.5	234	2	140822	sigk protein - C10
31	36	54.5	299	2	G72307	hypothetical prote
32	36	54.5	310	2	A33489	hypothetical prote
33	36	54.5	357	2	S21992	envelope protein 9
34	36	54.5	370	2	A05034	hypothetical prote
35	36	54.5	447	2	F81678	GTP-binding protei
36	36	54.5	484	2	A70558	hypothetical prote
37	36	54.5	499	2	G84972	leucyl aminopeptid
38	36	54.5	627	2	C82418	GCDF family prote
39	36	54.5	672	2	S46276	acetate-CoA ligase
40	36	54.5	760	2	T24521	hypothetical prote
41	36	54.5	780	2	AC1427	transcriptional regu
42	36	54.5	1014	2	T30840	serine-repeat anti
43	36	54.5	8243	2	T31307	type I fatty acid
44	35	53.0	62	1	R5H31F	ribosomal protein
45	35	53.0	98	2	T22503	hypothetical prote

ALIGNMENTS

RESULT 1

A99114
hypothetical protein orf125 [imported] - Giardia theta nucleomorph
C:Species: nucleomorph Giardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A99114

R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671; PMID:11323671
A:Accession: A99114

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <DOU>
A:Cross-references: UNIPROT:O9AVZ1; GB:A010592; NID:912580762; PIDN:CAC27080.1; GSPDB:
C:Genetics:
A:Gene: orf125
A:Map position: 2
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 63.6%; Score 42; DB 2; Length 125;
Best Local Similarity 70.0%; Pred. No. 7;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IRKIHIIKK 14
DB 9 IRKIHIVRK 18

RESULT 2

S68411
cathelin-related protein 2 precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S68411

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Calguri, D.J.; Huttner, K.M.
FEBS Lett. 377, 519-522, 1995
A:Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial)
A:Reference number: S68411; MUID:96140581; PMID:8549789
A:Accession: S68411

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-152 <MAH>
A:Cross-references: EMBL:X92757
C:Genetics:
A:Gene: SCS-2
C:Superfamily: cathelin; cystatin homology

F:1-21/Domain: signal sequence #stratus predicted <SIG>
F:14-122/Domain: cystatin homology <CTG>
F:21-123/Domain: propeptide #status predicted <PRO>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-12

Sequence: 1 LRRIRKIIHIHK 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA: *
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	14	US-10-060-102-13	Sequence 13, Appl
2	66	100.0	14	US-10-060-102-18	Sequence 18, Appl
3	66	100.0	14	US-10-721-839-13	Sequence 13, Appl
4	66	100.0	14	US-10-721-839-18	Sequence 18, Appl
5	66	100.0	16	US-10-060-102-14	Sequence 14, Appl
6	66	100.0	16	US-10-721-839-14	Sequence 14, Appl
7	66	100.0	18	US-09-840-009-2	Sequence 2, Appl
8	66	100.0	18	US-09-840-009-9	Sequence 9, Appl
9	66	100.0	18	US-09-840-009-16	Sequence 16, Appl
10	66	100.0	18	US-09-840-009-23	Sequence 23, Appl
11	66	100.0	18	US-09-840-009-30	Sequence 30, Appl
12	66	100.0	18	US-10-060-102-9	Sequence 9, Appl
13	66	100.0	18	US-10-060-102-12	Sequence 12, Appl

14	66	100.0	18	US-10-721-839-9	Sequence 9, Appl
15	66	100.0	18	US-10-721-839-12	Sequence 12, Appl
16	66	100.0	29	US-10-060-102-8	Sequence 8, Appl
17	66	100.0	29	US-10-721-839-8	Sequence 8, Appl
18	64	97.0	14	US-10-060-102-19	Sequence 19, Appl
19	64	97.0	14	US-10-060-102-19	Sequence 19, Appl
20	64	97.0	14	US-10-060-102-20	Sequence 20, Appl
21	64	97.0	14	US-10-721-839-19	Sequence 19, Appl
22	64	97.0	16	US-10-060-102-15	Sequence 20, Appl
23	64	97.0	16	US-10-721-839-15	Sequence 15, Appl
24	64	97.0	18	US-10-060-102-10	Sequence 10, Appl
25	64	97.0	18	US-10-060-102-11	Sequence 10, Appl
26	64	97.0	18	US-10-721-839-10	Sequence 11, Appl
27	64	97.0	18	US-10-721-839-11	Sequence 11, Appl
28	61	92.4	18	US-09-840-009-4	Sequence 8, Appl
29	61	92.4	18	US-09-840-009-8	Sequence 8, Appl
30	61	92.4	18	US-09-840-009-11	Sequence 11, Appl
31	61	92.4	18	US-09-840-009-15	Sequence 15, Appl
32	61	92.4	18	US-09-840-009-18	Sequence 18, Appl
33	61	92.4	18	US-09-840-009-22	Sequence 22, Appl
34	61	92.4	18	US-09-840-009-25	Sequence 25, Appl
35	61	92.4	18	US-09-840-009-29	Sequence 29, Appl
36	61	92.4	18	US-10-060-102-25	Sequence 25, Appl
37	61	92.4	18	US-10-721-839-25	Sequence 25, Appl
38	60	90.9	18	US-09-840-009-5	Sequence 5, Appl
39	60	90.9	18	US-09-840-009-12	Sequence 12, Appl
40	60	90.9	18	US-09-840-009-19	Sequence 19, Appl
41	60	90.9	18	US-09-840-009-26	Sequence 26, Appl
42	59	89.4	18	US-09-840-009-6	Sequence 6, Appl
43	59	89.4	18	US-09-840-009-7	Sequence 7, Appl
44	59	89.4	18	US-09-840-009-13	Sequence 13, Appl
45	59	89.4	18	US-09-840-009-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-060-102-13
Sequence 13, Application US/10060102
Publication No. US2003022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STRAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-13

Query Match 100.0%; Score 66; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRRIRKIIHIHK 14

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-12

Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	66	100.0	18	4	US-09-840-009-9
3	66	100.0	18	4	US-09-840-009-16
4	66	100.0	18	4	US-09-840-009-23
5	66	100.0	18	4	US-09-840-009-30
6	61	92.4	18	4	US-09-840-009-4
7	61	92.4	18	4	US-09-840-009-8
8	61	92.4	18	4	US-09-840-009-11
9	61	92.4	18	4	US-09-840-009-15
10	61	92.4	18	4	US-09-840-009-18
11	61	92.4	18	4	US-09-840-009-22
12	61	92.4	18	4	US-09-840-009-25
13	61	92.4	18	4	US-09-840-009-29
14	60	90.9	18	4	US-09-840-009-5
15	60	90.9	18	4	US-09-840-009-12
16	60	90.9	18	4	US-09-840-009-19
17	60	90.9	18	4	US-09-840-009-26
18	59	89.4	18	4	US-09-840-009-6
19	59	89.4	18	4	US-09-840-009-7
20	59	89.4	18	4	US-09-840-009-13
21	59	89.4	18	4	US-09-840-009-14
22	59	89.4	18	4	US-09-840-009-20
23	59	89.4	18	4	US-09-840-009-21
24	59	89.4	18	4	US-09-840-009-27
25	59	89.4	18	4	US-09-840-009-28
26	58	87.9	18	4	US-09-840-009-3
27	58	87.9	18	4	US-09-840-009-10

28	58	87.9	18	4	US-09-840-009-17	Sequence 17, Appl
29	58	87.9	18	4	US-09-840-009-24	Sequence 24, Appl
30	58	87.9	18	4	US-09-840-009-31	Sequence 31, Appl
31	58	87.9	18	4	US-09-840-009-34	Sequence 34, Appl
32	58	87.9	18	4	US-09-840-009-35	Sequence 35, Appl
33	50	75.8	18	4	US-09-840-009-32	Sequence 32, Appl
34	50	75.8	18	4	US-09-840-009-33	Sequence 33, Appl
35	50	75.8	18	4	US-09-840-009-36	Sequence 36, Appl
36	50	75.8	18	4	US-09-840-009-37	Sequence 37, Appl
37	46	69.7	18	4	US-09-840-009-1	Sequence 1, Appl
38	42	63.6	160	4	US-09-917-340-36	Sequence 36, Appl
39	41	62.1	337	4	US-09-538-092-38	Sequence 38, Appl
40	40	60.6	24	4	US-09-785-059B-5	Sequence 5, Appl
41	40	60.6	36	4	US-09-785-059B-6	Sequence 6, Appl
42	40	60.6	42	4	US-09-785-059B-7	Sequence 7, Appl
43	40	60.6	48	4	US-09-785-059B-8	Sequence 8, Appl
44	39	59.1	391	3	US-09-134-001C-5234	Sequence 5234, Ap
45	38	57.6	149	4	US-09-774-639-304	Sequence 304, App

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Marling, Alan J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840, 009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606, 858
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match
Best Local Similarity 100.0%; Score 66; DB 4; Length 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRRIRKIHIIKK 14
DB 3 LRRIRKIHIIKK 16
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Marling, Alan J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840, 009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606, 858
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-12

Perfect score: 66
Sequence: 1 LRRIRKRIHIIKK 14

Scoring table: BLOSUM62

Gap 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	14	4	AAb70658 Ovine SMA
2	66	100.0	14	4	AAb70659 Ovine SMA
3	66	100.0	14	5	ABP53280 Synthetic
4	66	100.0	14	5	ABP53285 Synthetic
5	66	100.0	16	4	AAb70656 Ovine SMA
6	66	100.0	16	5	ABP53281 Synthetic
7	66	100.0	18	4	AAb70655 Ovine SMA
8	66	100.0	18	4	AAb70648 Ovine SMA
9	66	100.0	18	5	AAE20882 D11-novi
10	66	100.0	18	5	AAE20875 D11-novi
11	66	100.0	18	5	AAE20854 Ovi-splatin
12	66	100.0	18	5	AAE20861 D16-novis
13	66	100.0	18	5	AAE20868 D17-novis
14	66	100.0	18	5	ABP53276 Synthetic
15	66	100.0	18	5	ABP53279 Synthetic
16	66	100.0	29	5	ABP53275 Synthetic
17	66	100.0	29	5	ABP53275 Synthetic
18	66	97.0	14	4	AAb70661 Ovine SMA
19	66	97.0	14	4	AAb70660 Ovine SMA
20	66	97.0	14	5	ABP53286 Synthetic
21	66	97.0	14	5	ABP53287 Synthetic
22	66	97.0	16	4	AAb70657 Ovine SMA
23	66	97.0	16	5	ABP53282 Synthetic
24	66	97.0	18	4	AAb70654 Ovine SMA
25	66	97.0	18	5	ABP53278 Synthetic

26	64	97.0	18	5	ABP53277 Synthetic
27	64	97.0	20	4	AAb70653 Ovine SMA
28	62	93.9	13	4	AAb70663 Ovine SMA
29	61	92.4	13	4	AAb70662 Ovine SMA
30	61	92.4	18	5	AAE20870
31	61	92.4	18	5	AAE20860
32	61	92.4	18	5	AAE20881 DA11-novi
33	61	92.4	18	5	AAE20867 DA7-novis
34	61	92.4	18	5	AAE20874 DA10-novi
35	61	92.4	18	5	AAE20863 T7-novisp
36	61	92.4	18	5	AAE20877 T11-novisp
37	61	92.4	18	5	AAE20856 T6-novisp
38	61	92.4	18	5	ABP53292 Synthetic
39	60	90.9	18	5	AAE20864 S7-novisp
40	60	90.9	18	5	AAE20871 S10-novisp
41	60	90.9	18	5	AAE20878 S11-novisp
42	60	90.9	18	5	AAE20857 S6-novisp
43	59	89.4	18	5	AAE20872 E10-novis
44	59	89.4	18	5	AAE20873 D10-novis
45	59	89.4	18	5	AAE20858 E6-novisp

ALIGNMENTS

RESULT 1	AAb70658	standard; peptide; 14 AA.
ID	AAb70658	
XX	AAb70658	
AC	AAb70658	
XX	AAb70658	
DT	15-MAY-2001	(first entry)
XX	15-MAY-2001	
DE	Ovine SMAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:11.	
XX	Ovine SMAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:11.	
KW	Ovine, SMAP29; lupine, RCAP 18; cathelicidin; antimicrobial; bactericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Xanthomonas.	
KM	Ovis aries.	
OS	Ovis aries.	
XX	WO200112668-A1.	
PN	22-FEB-2001.	
XX	22-FEB-2001.	
PD	18-AUG-2000; 2000MO-US022781.	
XX	18-AUG-2000; 2000MO-US022781.	
PR	18-AUG-1999; 99US-0149886P.	
XX	18-AUG-1999; 99US-0149886P.	
PA	(IOWA) UNIV IOWA RES FOUND.	
XX	(REGC) UNIV CALIFORNIA.	
PI	Tack BE, Mccrery P, Welsh M, Travis SM, Lehrer R;	
XX	WPI; 2001-234911/24.	
DR	New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections.	
XX	Claim 1, Page 103; 137p; English.	
PT	AAb70648 to AAb70675 represent antimicrobial peptides (I), of which	
XX	AAb70648 to AAb70675 represent antimicrobial peptides (I), of which	
CC	SMAP 29 cathelicidin family peptide, and AAb70675 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antitumor and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (II) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas	

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:06 ; Search time 43.6816 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-11
Perfect score: 66
Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	65.2	638	2	Q8D796
2	43	65.2	660	2	Q7MEAO
3	42	63.6	125	2	Q9AVZ1
4	42	63.6	160	1	SCS1_SHEEP
5	42	63.6	160	1	SCS2_SHEEP
6	42	63.6	308	2	Q8RC7
7	42	63.6	500	1	TF3B_SCHPO
8	41	62.1	41	2	Q48971
9	41	62.1	217	2	Q977R2
10	41	62.1	337	1	YBZ1_YEAST
11	41	62.1	414	2	Q947U2
12	41	62.1	414	2	Q7XEY8
13	41	62.1	613	1	DEAD_HAEIN
14	41	62.1	670	1	REP_BUCBP
15	40	60.6	256	2	Q83CP2
16	40	60.6	370	2	O67743
17	40	60.6	452	2	Q7N787
18	40	60.6	461	2	Q8IBM2
19	40	60.6	475	2	Q7SGI8
20	40	60.6	867	2	O28391
21	39	59.1	202	1	HAM1_AQUAE
22	39	59.1	210	2	Q92CLS
23	39	59.1	250	2	Q7W5P0
24	39	59.1	250	2	Q7WCY5
25	39	59.1	258	2	Q8MY71
26	39	59.1	349	2	Q736D5
27	39	59.1	349	2	O81P89
28	39	59.1	349	2	O6HHI2
29	39	59.1	407	2	Q9UTH1
30	39	59.1	428	2	O8TXS5
31	39	59.1	483	2	O9KR81

32	39	59.1	598	2	Q7VTH0	Q7VTH0 bordetella
33	39	59.1	838	2	Q9DYL4	Q9DYL4 human immun
34	39	59.1	903	2	Q9SWA7	Q9SWA7 bulla goud
35	39	59.1	967	2	Q7R084	Q7R084 plasmidium
36	39	59.1	1157	2	Q7RON5	Q7RON5 plasmidium
37	39	59.1	1160	2	Q7SBL3	Q7SBL3 neurospora
38	39	59.1	1226	2	O6LS73	O6LS73 oryza sativ
39	39	59.1	1580	2	Q7RMP4	Q7RMP4 plasmidium
40	39	59.1	2084	2	O8ILJ6	O8ILJ6 plasmidium
41	39	59.1	4057	2	O8IUE7	O8IUE7 plasmidium
42	38	57.6	87	1	SSS1_SCYCA	SSS1_SCYCA scylothrinu
43	38	57.6	102	2	O8Y3R8	O8Y3R8 listeria mo
44	38	57.6	102	2	O926Y2	O926Y2 listeria mo
45	38	57.6	102	2	Q71VZ6	Q71VZ6 listeria mo

ALIGNMENTS

RESULT 1
Q8D796 PRELIMINARY; PRT; 638 AA.
ID Q8D796;
AC Q8D796;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Predicted signal transduction protein.
GN OrderedLocusNames=V20264;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AE016808; AA007230.1; --
DR InterPro; IPR001633; EAL.
DR InterPro; IPR003018; GDEF.
DR InterPro; IPR000160; GDEF.
DR Pfam; PF00563; EAL; 1.
DR Pfam; PF00563; GDEF; 1.
DR Pfam; PF00563; GDEF; 1.
DR Pfam; PF00563; GDEF; 1.
DR SMART; SM00052; DUF2; 1.
DR SMART; SM00052; DUF2; 1.
DR TIGRFAMs; TIGR0254; GDEF; 1.
DR PROSITE; PS50883; EAL; 1.
DR PROSITE; PS50887; GDEF; 1.
KW Complete proteome.
SQ SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64;
Query Match 65.2%; Score 43; DB 2; Length 638;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 RRIIRKIHIIKK 14
Db 566 KEIRSIHVAKK 578
RESULT 2
ID Q7MEAO PRELIMINARY; PRT; 660 AA.
AC Q7MEAO;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE GDBF family protein.
GN OrderedLocusNames=VVA0770;
OS Vibrio vulnificus (strain VJ016).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-11
Perfect score: 66
Sequence: 1 LRRIRKIH1IKK 14

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 33106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	66	100.0	14	US-10-060-102-13
2	66	100.0	14	US-10-060-102-13
3	66	100.0	14	US-10-060-102-13
4	66	100.0	14	US-10-721-839-13
5	66	100.0	14	US-10-721-839-13
6	66	100.0	16	US-10-060-102-14
7	66	100.0	16	US-10-721-839-14
8	66	100.0	18	US-09-840-009-2
9	66	100.0	18	US-09-840-009-9
10	66	100.0	18	US-09-840-009-16
11	66	100.0	18	US-09-840-009-23
12	66	100.0	18	US-09-840-009-30
13	66	100.0	18	US-10-060-102-9
			18	US-10-060-102-12

14	66	100.0	18	US-10-721-839-9	Sequence 9, Appl1
15	66	100.0	18	US-10-721-839-12	Sequence 12, Appl1
16	66	100.0	29	US-10-060-102-8	Sequence 8, Appl1
17	66	100.0	29	US-10-721-839-8	Sequence 8, Appl1
18	64	97.0	14	US-10-060-102-19	Sequence 19, Appl1
19	64	97.0	14	US-10-060-102-20	Sequence 20, Appl1
20	64	97.0	14	US-10-721-839-19	Sequence 19, Appl1
21	64	97.0	14	US-10-721-839-20	Sequence 20, Appl1
22	64	97.0	16	US-10-721-839-15	Sequence 15, Appl1
23	64	97.0	16	US-10-060-102-15	Sequence 15, Appl1
24	64	97.0	18	US-10-060-102-10	Sequence 10, Appl1
25	64	97.0	18	US-10-060-102-11	Sequence 11, Appl1
26	64	97.0	18	US-10-060-102-11	Sequence 11, Appl1
27	64	97.0	18	US-10-721-839-11	Sequence 11, Appl1
28	61	92.4	18	US-09-840-009-4	Sequence 4, Appl1
29	61	92.4	18	US-09-840-009-8	Sequence 8, Appl1
30	61	92.4	18	US-09-840-009-11	Sequence 11, Appl1
31	61	92.4	18	US-09-840-009-15	Sequence 15, Appl1
32	61	92.4	18	US-09-840-009-18	Sequence 18, Appl1
33	61	92.4	18	US-09-840-009-22	Sequence 22, Appl1
34	61	92.4	18	US-09-840-009-25	Sequence 25, Appl1
35	61	92.4	18	US-09-840-009-29	Sequence 29, Appl1
36	61	92.4	18	US-10-060-102-25	Sequence 25, Appl1
37	61	92.4	18	US-10-721-839-25	Sequence 25, Appl1
38	60	90.9	18	US-09-840-009-5	Sequence 5, Appl1
39	60	90.9	18	US-09-840-009-12	Sequence 12, Appl1
40	60	90.9	18	US-09-840-009-19	Sequence 19, Appl1
41	60	90.9	18	US-09-840-009-26	Sequence 26, Appl1
42	59	89.4	18	US-09-840-009-6	Sequence 6, Appl1
43	59	89.4	18	US-09-840-009-7	Sequence 7, Appl1
44	59	89.4	18	US-09-840-009-13	Sequence 13, Appl1
45	59	89.4	18	US-09-840-009-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-10-060-102-13
Sequence 13, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STABLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA.035US
CURRENT APPLICATION NUMBER: US/10/060,102
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-13
OTHER INFORMATION: Peptide

Query Match Best Local Similarity 100.0%; Score 66; DB 14; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRRIRKIH1IKK 14

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-11

Perfect score: 66

Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep.*
5: /cgn2_6/prodata/1/1aa/6C COMB.pep.*
6: /cgn2_6/prodata/1/1aa/6D COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	18	4	US-09-840-009-2
2	66	100.0	18	4	US-09-840-009-9
3	66	100.0	18	4	US-09-840-009-16
4	66	100.0	18	4	US-09-840-009-23
5	66	100.0	18	4	US-09-840-009-30
6	61	92.4	18	4	US-09-840-009-4
7	61	92.4	18	4	US-09-840-009-8
8	61	92.4	18	4	US-09-840-009-11
9	61	92.4	18	4	US-09-840-009-15
10	61	92.4	18	4	US-09-840-009-18
11	61	92.4	18	4	US-09-840-009-22
12	61	92.4	18	4	US-09-840-009-25
13	61	92.4	18	4	US-09-840-009-29
14	60	90.9	18	4	US-09-840-009-5
15	60	90.9	18	4	US-09-840-009-12
16	60	90.9	18	4	US-09-840-009-19
17	60	90.9	18	4	US-09-840-009-26
18	59	89.4	18	4	US-09-840-009-7
19	59	89.4	18	4	US-09-840-009-13
20	59	89.4	18	4	US-09-840-009-14
21	59	89.4	18	4	US-09-840-009-20
22	59	89.4	18	4	US-09-840-009-21
23	59	89.4	18	4	US-09-840-009-27
24	59	89.4	18	4	US-09-840-009-28
25	59	89.4	18	4	US-09-840-009-3
26	58	87.9	18	4	US-09-840-009-10
27	58	87.9	18	4	US-09-840-009-17

28	58	87.9	18	4	US-09-840-009-17	Sequence 17, Appl
29	58	87.9	18	4	US-09-840-009-24	Sequence 24, Appl
30	58	87.9	18	4	US-09-840-009-31	Sequence 31, Appl
31	58	87.9	18	4	US-09-840-009-35	Sequence 35, Appl
32	58	87.9	18	4	US-09-840-009-32	Sequence 32, Appl
33	50	75.8	18	4	US-09-840-009-33	Sequence 33, Appl
34	50	75.8	18	4	US-09-840-009-36	Sequence 36, Appl
35	50	75.8	18	4	US-09-840-009-37	Sequence 37, Appl
36	50	75.8	18	4	US-09-840-009-38	Sequence 38, Appl
37	46	69.7	18	4	US-09-840-009-39	Sequence 39, Appl
38	42	63.6	160	4	US-09-917-340-36	Sequence 36, Appl
39	41	62.1	337	4	US-09-538-092-38	Sequence 38, Appl
40	40	60.6	24	4	US-09-785-0598-5	Sequence 5, Appl1
41	40	60.6	36	4	US-09-785-0598-6	Sequence 6, Appl1
42	40	60.6	42	4	US-09-785-0598-7	Sequence 7, Appl1
43	40	60.6	48	4	US-09-785-0598-8	Sequence 8, Appl1
44	39	59.1	391	3	US-09-134-001C-5234	Sequence 5234, Ap
45	38	57.6	149	4	US-09-774-639-304	Sequence 304, App

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVIAPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match 100.0%, Score 66, DB 4, Length 18,
Best Local Similarity 100.0%, Pred. No. 0.00036,
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 LRRIRKIHIIKK 14
DB 3 LRRIRKIHIIKK 16
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVIAPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds

(without alignment)
110.327 Million cell updates/sec

Title: US-09-642-744D-11
Perfect score: 66
Sequence: 1 LRRIRKIHIXK 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	14	4 AAB70658	Aab70658 Ovine SMA
2	66	100.0	14	4 AAB70659	Aab70659 Ovine SMA
3	66	100.0	14	5 ABP53280	Abp53280 Synthetic
4	66	100.0	14	5 ABP53285	Abp53285 Synthetic
5	66	100.0	16	4 AAB70656	Aab70656 Ovine SMA
6	66	100.0	16	5 ABP53281	Abp53281 Synthetic
7	66	100.0	18	4 AAB70655	Aab70655 Ovine SMA
8	66	100.0	18	4 AAB70648	Aab70648 Ovine SMA
9	66	100.0	18	5 AAE20882	Aae20882 D11-nov1
10	66	100.0	18	5 AAE20885	Aae20885 D11-nov1
11	66	100.0	18	5 AAE20854	Aae20854 Ovisplrin
12	66	100.0	18	5 AAE20861	Aae20861 D16-nov1s
13	66	100.0	18	5 AAE20868	Aae20868 D17-nov1s
14	66	100.0	18	5 ABP53276	Abp53276 Synthetic
15	66	100.0	18	5 ABP53279	Abp53279 Synthetic
16	66	100.0	29	4 AAB70675	Aab70675 Ovine SMA
17	66	100.0	29	5 ABP53275	Abp53275 Synthetic
18	64	97.0	14	4 AAB70661	Aab70661 Ovine SMA
19	64	97.0	14	4 AAB70660	Aab70660 Ovine SMA
20	64	97.0	14	5 ABP53286	Abp53286 Synthetic
21	64	97.0	14	5 ABP53287	Abp53287 Synthetic
22	64	97.0	16	4 AAB70657	Aab70657 Ovine SMA
23	64	97.0	16	5 ABP53282	Abp53282 Synthetic
24	64	97.0	18	4 AAB70654	Aab70654 Ovine SMA
25	64	97.0	18	5 ABP53278	Abp53278 Synthetic

ALIGNMENTS

26	64	97.0	18	5 ABP53277	Abp53277 Synthetic
27	64	97.0	20	4 AAB70653	Aab70653 Ovine SMA
28	62	93.9	13	4 AAB70663	Aab70663 Ovine SMA
29	61	92.4	13	4 AAB70662	Aab70662 Ovine SMA
30	61	92.4	18	5 AAE20870	Aae20870 D10-nov1s
31	61	92.4	18	5 AAE20860	Aae20860 D16-nov1s
32	61	92.4	18	5 AAE20881	Aae20881 D11-nov1s
33	61	92.4	18	5 AAE20867	Aae20867 D17-nov1s
34	61	92.4	18	5 AAE20874	Aae20874 D10-nov1
35	61	92.4	18	5 AAE20863	Aae20863 T7-nov1sp
36	61	92.4	18	5 AAE20877	Aae20877 T11-nov1s
37	61	92.4	18	5 AAE20856	Aae20856 T6-nov1sp
38	60	90.9	18	5 ABP53292	Abp53292 Synthetic
39	60	90.9	18	5 AAE20864	Aae20864 S7-nov1sp
40	60	90.9	18	5 AAE20871	Aae20871 S10-nov1s
41	60	90.9	18	5 AAE20878	Aae20878 S11-nov1s
42	60	90.9	18	5 AAE20857	Aae20857 S6-nov1sp
43	59	89.4	18	5 AAE20872	Aae20872 E10-nov1s
44	59	89.4	18	5 AAE20873	Aae20873 D10-nov1s
45	59	89.4	18	5 AAE20858	Aae20858 E6-nov1sp

RESULT 1

AAB70658
ID AAB70658 standard; peptide; 14 AA.

XX AAB70658;

DT 15-MAY-2001 (first entry)

DE Ovine SMAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:11.

XX Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;

KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;

KM proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

XX Burkholderia cepacia; Alcaligenes; Xanthomonas.

OS Ovis aries.

XX WO200112668-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022781.

XX 18-AUG-1999; 99US-0149886P.

XX (IOWA) UNIV IOWA RES FOUNO.

XX (REGC) UNIV CALIFORNIA.

XX Tack BE, Mccrory P, Welsh M, Travis SM, Lehrer R;

XX WPI; 2001-234911/24.

XX New antimicrobial peptides useful as antibiotics for inhibiting growth

XX and proliferation of microbes, and for treating microbial infections.

XX Claim 1; Page 103; 137pp; English.

XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which

XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine

XX SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived

XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,

XX antimicrobial and antiviral activities, and can be used as microbial

XX growth and proliferation inhibitors and in gene therapy. (I) are useful

XX for inhibiting microbial growth in an environment capable of sustaining

XX such growth, for inhibiting microbial growth or strain in a host, and

XX inhibiting the growth of drug-resistant microbial strains such as

XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 49.9218 seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-10

Perfect score: 79

Sequence: 1 NRRIRKIIHIITKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Litering first 45 summaries

Database : UniProt_03.*
1: uniProt_sprot.*
2: uniProt_trembl.*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	60.8	500	1	TF3B_SCHPO
2	47	59.5	160	1	SC51_SHEEP
3	47	59.5	160	1	SC52_SHEEP
4	45	57.0	182	2	Q896E1
5	45	57.0	234	2	Q59264
6	45	57.0	308	2	Q8R2C7
7	45	57.0	834	2	Q7RRI0
8	44	55.7	231	2	Q8RAG4
9	44	55.7	233	2	Q9L7X2
10	44	55.7	233	2	Q8XJ18
11	44	55.7	349	2	Q736D5
12	44	55.7	349	2	Q81P89
13	44	55.7	349	2	Q6HHI2
14	44	55.7	402	2	Q81I43
15	44	55.7	420	1	PR11_HUMAN
16	44	55.7	460	2	Q9VL03
17	44	55.7	549	2	Q81PC2
18	44	55.7	1137	2	Q6LFF7
19	44	55.7	1279	2	Q81B12
20	44	55.7	2084	2	Q81B12
21	44	55.7	6077	2	Q6LFF6
22	43	54.4	483	2	P95941
23	43	54.4	638	2	Q8D796
24	43	54.4	660	2	Q7MEAO
25	43	54.4	867	2	Q28391
26	43	54.4	875	2	Q8R8R4
27	43	54.4	878	2	Q7RY40
28	43	54.4	3267	2	Q81B20
29	42.5	53.8	301	2	Q7Q4C0
30	42.5	53.8	314	2	Q65L76
31	42.5	53.8	324	2	Q62X75

32	42	53.2	125	2	Q9AV21	Q9AV21 guillardi
33	42	53.2	146	1	RUVX_MYCPU	Q98G13 mycoplasma
34	42	53.2	151	2	Q8R8S1	Q8R8S1 thermomane
35	42	53.2	157	2	Q7NA14	Q7NA14 photorhabd
36	42	53.2	198	2	Q6LIE8	Q6LIE8 picophiliu
37	42	53.2	232	2	Q7MTQ1	Q7MTQ1 porphyromon
38	42	53.2	414	2	Q947U2	Q947U2 oryza activ
39	42	53.2	414	2	Q7XEV8	Q7XEV8 oryza activ
40	42	53.2	415	2	Q89045	Q89045 ractus noty
41	42	53.2	417	1	PR11_MOUSE	P20664 mus musculu
42	42	53.2	530	2	Q9C2F6	Q9C2F6 neurospora
43	42	53.2	537	2	Q97WL6	Q97WL6 sulfolobus
44	42	53.2	678	2	Q7PDP0	Q7PDP0 anopheles g
45	42	53.2	684	2	Q7QNN1	Q7QNN1 giardia lam

ALIGNMENTS

RESULT 1
TF3B_SCHPO STANDARD; PRT; 500 AA.
AC Q9P6R0; Q9USU4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transcription factor IIB 60 kDa subunit (TFIIB) (B-related factor)
DE (BRF) (TFIIB-related factor).
GN Name=brfl; ORFNames=SPBC13E7.10c, SPBC30D10.20;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_Taxid=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward K., Volkart G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Welford J., Vancutsem E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinbach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Motier S.,
RA Gilbert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez J., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nure P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
[2]
INTERACTION WITH TBP.
RX MEDLINE=22569152; PubMed=12682361; DOI=10.1093/nar/gkq301;
RA Huang Y., McGillicuddy E., Weindl M., Dong S., Marata R.J.;
RT "The fission yeast TFIIB-related factor limits RNA polymerase III to a
TBP-dependent pathway of TBP recruitment.";
RL Nucleic Acids Res. 31:2108-2116(2003).
CC -1- FUNCTION: General activator of RNA polymerase III transcription.
CC -1- COPACITOR: Binds 1 zinc ion per subunit (By similarity).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 9.92179 Seconds
(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-10

Sequence: 1 NTRRIIRKIHIHKY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pirl:1:
2: pirl:2:
3: pirl:3:
4: pirl:4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	59.5	152	2	S68411 cathelin-related p
2	47	59.5	160	2	S68412 cathelin-related p
3	47	59.5	160	2	S68228 myeloid antimicrob
4	45	57.0	234	2	D97108 DNA-dependent RNA
5	45	57.0	234	2	D97108 DNA-dependent RNA
6	44	55.7	420	2	S45630 DNA primase chain
7	43	54.4	483	2	S75369 DNA-directed RNA p
8	43	54.4	483	2	S75369 DNA-directed RNA p
9	42	53.2	125	2	A89114 hypotheical prote
10	42	53.2	146	2	D90811 conserved hypothe
11	42	53.2	146	2	D90811 conserved hypothe
12	42	53.2	146	2	D90811 conserved hypothe
13	42	53.2	146	2	D90811 conserved hypothe
14	41	51.9	186	2	B90116 hypotheical prote
15	41	51.9	337	2	S46010 hypotheical prote
16	41	51.9	507	2	T10753 intestinal DNA rep
17	41	51.9	613	2	F64056 probable ATP-depen
18	40	50.6	105	2	F71128 hypotheical prote
19	40	50.6	177	2	T28362 hypotheical prote
20	40	50.6	221	2	S39609 EBD2 proteain - mal
21	40	50.6	370	2	C70464 GTP-binding protei
22	40	50.6	791	2	D82901 ATP-dependent prot
23	40	50.6	1634	2	E64410 DNA-directed DNA p
24	39.5	50.0	1741	2	T15978 hypotheical prote
25	39.5	50.0	208	2	G81196 N-(5'-phosphoribos
26	39.5	50.0	208	2	G81196 N-(5'-phosphoribos
27	39.5	50.0	313	2	A89971 cmp-binding-factor
28	39	49.4	41	2	S7768 hypotheical prote
29	39	49.4	113	2	G90223 DNA-directed RNA p
30	39	49.4	151	2	H90035 tear transcription

30	39	49.4	202	1	H70318 conserved hypothet
31	39	49.4	210	2	AC1577 precortin isomeras
32	39	49.4	292	2	A97035 cation efflux syst
33	39	49.4	319	1	S19248 RNA-directed DNA p
34	39	49.4	334	2	B72301 endoglucanase - Th
35	39	49.4	407	2	T17888 hypotheical prote
36	39	49.4	414	2	G64091 cell division prot
37	39	49.4	483	2	B82160 hypotheical prote
38	39	49.4	540	2	T33982 hypotheical prote
39	39	49.4	762	2	S56141 HAKI protein - Yea
40	38.5	48.7	381	1	C64416 conserved hypothet
41	38	48.1	87	2	S00180 spermatid protein
42	38	48.1	96	2	C64354 hypotheical prote
43	38	48.1	156	1	D71689 ORF MSV127 hypothe
44	38	48.1	172	2	T28288 transcription regu
45	38	48.1	189	2	H96903

ALIGNMENTS

RESULT 1

S68411

cathelin-related protein 2 precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68411

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Hutter, K.M.

FEBS Lett. 377, 519-522, 1995

A>Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411, MUID:96140581, PMID:8549789

A/Accession: S68411

A>Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-152 <MAH>

A/Cross-references: EMBL:X92757

C/Genetics:

A:Gene: SCS-2

C/Superfamily: cathelin, cystatin homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:14-122/Domain: cystatin homology <CYS>

F:121-123/Domain: propeptide #status predicted <PRO>

F:124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match

Best Local Similarity 59.5%; Score 47; DB 2; Length 152;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 2

S68412

cathelin-related protein 1 precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68412

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Hutter, K.M.

FEBS Lett. 377, 519-522, 1995

A>Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411, MUID:96140581, PMID:8549789

A/Accession: S68412

A>Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-150 <MAH>

A/Cross-references: EMBL:X92758

C/Genetics:

A:Gene: SCS-1

C/Superfamily: cathelin, cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:122-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 43.5307 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-10

Sequence: 1 NRRIRKTHIKKY 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*

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19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	79	100.0	16	14	US-10-060-102-15
2	79	100.0	16	15	US-10-721-839-15
3	79	100.0	16	15	US-10-060-102-10
4	79	100.0	16	14	US-10-060-102-11
5	79	100.0	16	15	US-10-721-839-10
6	79	100.0	16	15	US-10-721-839-11
7	77	97.5	16	14	US-10-060-102-14
8	77	97.5	16	15	US-10-721-839-14
9	77	97.5	16	9	US-09-840-009-2
10	77	97.5	16	9	US-09-840-009-9
11	77	97.5	16	9	US-09-840-009-16
12	77	97.5	16	9	US-09-840-009-23
13	77	97.5	16	9	US-09-840-009-30

14	77	97.5	18	14	US-10-060-102-9	Sequence 9, Appl1
15	77	97.5	18	14	US-10-060-102-12	Sequence 12, Appl1
16	77	97.5	18	15	US-10-721-839-9	Sequence 9, Appl1
17	77	97.5	18	15	US-10-721-839-12	Sequence 12, Appl1
18	77	97.5	29	14	US-10-060-102-8	Sequence 8, Appl1
19	77	97.5	29	15	US-10-721-839-8	Sequence 8, Appl1
20	72	91.1	18	9	US-09-840-009-4	Sequence 4, Appl1
21	72	91.1	18	9	US-09-840-009-8	Sequence 8, Appl1
22	72	91.1	18	9	US-09-840-009-11	Sequence 11, Appl1
23	72	91.1	18	9	US-09-840-009-15	Sequence 15, Appl1
24	72	91.1	18	9	US-09-840-009-18	Sequence 18, Appl1
25	72	91.1	18	9	US-09-840-009-22	Sequence 22, Appl1
26	72	91.1	18	9	US-09-840-009-25	Sequence 25, Appl1
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28	72	91.1	18	14	US-10-060-102-25	Sequence 25, Appl1
29	72	91.1	18	15	US-10-721-839-25	Sequence 25, Appl1
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31	71	89.9	18	9	US-09-840-009-12	Sequence 12, Appl1
32	71	89.9	18	9	US-09-840-009-19	Sequence 19, Appl1
33	71	89.9	18	9	US-09-840-009-26	Sequence 26, Appl1
34	70	88.6	18	9	US-09-840-009-6	Sequence 6, Appl1
35	70	88.6	18	9	US-09-840-009-7	Sequence 7, Appl1
36	70	88.6	18	9	US-09-840-009-13	Sequence 13, Appl1
37	70	88.6	18	9	US-09-840-009-14	Sequence 14, Appl1
38	70	88.6	18	9	US-09-840-009-20	Sequence 20, Appl1
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41	70	88.6	18	9	US-09-840-009-28	Sequence 28, Appl1
42	69	87.3	18	9	US-09-840-009-3	Sequence 3, Appl1
43	69	87.3	18	9	US-09-840-009-10	Sequence 10, Appl1
44	69	87.3	18	9	US-09-840-009-17	Sequence 17, Appl1
45	69	87.3	18	9	US-09-840-009-24	Sequence 24, Appl1

ALIGNMENTS

RESULT 1

US-10-060-102-15

Sequence 15, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STAPLETON, JACK

APPLICANT: ROLLER, RICHARD

APPLICANT: STINSKI, MARK

APPLICANT: MCCRAY, PAUL B.

APPLICANT: TRICK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL

FILE REFERENCE: CATHELICIDINS

CURRENT APPLICATION NUMBER: US/10/060,102

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/265,270

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-060-102-15

Query Match 100.0%; Score 79; DB 14; Length 16;

Best Local Similarity 100.0%; Pred. No. 1,1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NRRIRKTHIKKY 16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 15.1955 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-10

Perfect score: 79

Sequence: 1 NRRIRKIHIIKKY 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	97.5	18	4	US-09-840-009-2
2	77	97.5	18	4	US-09-840-009-9
3	77	97.5	18	4	US-09-840-009-16
4	77	97.5	18	4	US-09-840-009-23
5	77	97.5	18	4	US-09-840-009-30
6	72	91.1	18	4	US-09-840-009-4
7	72	91.1	18	4	US-09-840-009-8
8	72	91.1	18	4	US-09-840-009-11
9	72	91.1	18	4	US-09-840-009-15
10	72	91.1	18	4	US-09-840-009-18
11	72	91.1	18	4	US-09-840-009-22
12	72	91.1	18	4	US-09-840-009-25
13	72	91.1	18	4	US-09-840-009-29
14	71	89.9	18	4	US-09-840-009-5
15	71	89.9	18	4	US-09-840-009-12
16	71	89.9	18	4	US-09-840-009-19
17	71	89.9	18	4	US-09-840-009-26
18	70	88.6	18	4	US-09-840-009-6
19	70	88.6	18	4	US-09-840-009-7
20	70	88.6	18	4	US-09-840-009-13
21	70	88.6	18	4	US-09-840-009-14
22	70	88.6	18	4	US-09-840-009-20
23	70	88.6	18	4	US-09-840-009-21
24	70	88.6	18	4	US-09-840-009-27
25	70	88.6	18	4	US-09-840-009-28
26	69	87.3	18	4	US-09-840-009-3
27	69	87.3	18	4	US-09-840-009-10

28	69	87.3	18	4	US-09-840-009-17	Sequence 17, Appl
29	69	87.3	18	4	US-09-840-009-24	Sequence 24, Appl
30	69	87.3	18	4	US-09-840-009-31	Sequence 31, Appl
31	63	79.7	18	4	US-09-840-009-34	Sequence 34, Appl
32	63	79.7	18	4	US-09-840-009-35	Sequence 35, Appl
33	61	77.2	18	4	US-09-840-009-32	Sequence 32, Appl
34	61	77.2	18	4	US-09-840-009-33	Sequence 33, Appl
35	57	72.2	18	4	US-09-840-009-1	Sequence 1, Appl
36	55	69.6	18	4	US-09-840-009-36	Sequence 36, Appl
37	55	69.6	18	4	US-09-840-009-37	Sequence 37, Appl
38	47	59.5	160	4	US-09-917-340-36	Sequence 36, Appl
39	47	59.5	169	4	US-09-270-767-35406	Sequence 35406, A
40	47	59.5	169	4	US-09-270-767-350623	Sequence 350623, A
41	43	54.4	66	4	US-09-270-767-39626	Sequence 39626, A
42	43	54.4	66	4	US-09-270-767-54843	Sequence 54843, A
43	42	53.2	24	4	US-09-785-0598-5	Sequence 5, Appl
44	42	53.2	36	4	US-09-785-0598-6	Sequence 6, Appl
45	42	53.2	42	4	US-09-785-0598-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          97.5%; Score 77; DB 4; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NRRIRKIHIIKKY 16
Db 2 NRRIRKIHIIKKY 17
RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:55 ; Search time 56.0894 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-10

Perfect score: 79

Sequence: 1 NRRIRKIHIMKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seque, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	4	ABP70657 Ovine SMA
2	79	100.0	16	5	ABP53282 Synthetic
3	79	100.0	18	4	ABP70654 Ovine SMA
4	79	100.0	18	5	ABP53278 Synthetic
5	79	100.0	18	5	ABP53277 Synthetic
6	79	100.0	20	4	ABP70653 Ovine SMA
7	77	97.5	16	4	ABP70656 Ovine SMA
8	77	97.5	16	5	ABP53281 Synthetic
9	77	97.5	18	4	ABP70655 Synthetic
10	77	97.5	18	4	ABP70648 Ovine SMA
11	77	97.5	18	5	ABP53282 Synthetic
12	77	97.5	18	5	ABP53276 Synthetic
13	77	97.5	18	5	ABP53279 Synthetic
14	77	97.5	18	5	ABP53275 Synthetic
15	77	97.5	18	5	ABP53278 Synthetic
16	77	97.5	18	5	ABP53277 Synthetic
17	77	97.5	18	5	ABP53276 Synthetic
18	77	97.5	18	5	ABP53279 Synthetic
19	77	97.5	18	5	ABP53275 Synthetic
20	77	97.5	18	5	ABP53278 Synthetic
21	77	97.5	18	5	ABP53277 Synthetic
22	77	97.5	18	5	ABP53276 Synthetic
23	77	97.5	18	5	ABP53279 Synthetic
24	77	97.5	18	5	ABP53275 Synthetic
25	77	97.5	18	5	ABP53278 Synthetic

26	72	91.1	18	5	AAE20877 T11-novis
27	72	91.1	18	5	AAE20856 T6-novisp
28	72	91.1	18	5	ABP53292 Synthetic
29	71	89.9	18	5	AAE20864 S7-novisp
30	71	89.9	18	5	AAE20871 S10-novis
31	71	89.9	18	5	AAE20878 S11-novis
32	71	89.9	18	5	AAE20857 S6-novisp
33	70	88.6	18	5	AAE20872 S10-novis
34	70	88.6	18	5	AAE20873 D10-novis
35	70	88.6	18	5	AAE20858 B6-novisp
36	70	88.6	18	5	AAE20866 D7-novisp
37	70	88.6	18	5	AAE20879 E11-novis
38	70	88.6	18	5	AAE20865 E7-novisp
39	70	88.6	18	5	AAE20880 D6-novisp
40	70	88.6	18	5	AAE20859 D5-novisp
41	69	87.3	18	5	AAE20862 G7-novisp
42	69	87.3	18	5	AAE20876 G11-novis
43	69	87.3	18	5	AAE20883 G10-novis
44	69	87.3	18	5	AAE20869 G10-novis
45	69	87.3	18	5	AAE20855 G6-novisp

ALIGNMENTS

RESULT 1
AAB70657 standard; peptide; 16 AA.

15-MAY-2001 (first entry)

Ovine SWAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:10.

Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial; bactericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Xanthomonas.

Ovis aries.

WO200112668-A1.

22-FEB-2001.

18-AUG-2000; 2000WO-US022781.

18-AUG-1999; 99US-0149886P.

(IOWA) UNIV IOWA RES FOUND.

(REGC) UNIV CALIFORNIA.

Tack BE, McCray P, Welsh M, Travis SM, Lehrer R; WPI; 2001-234911/24.

New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections.

Claim 1, Page 103; 137p; English.

AAE20877 T11-novis
Aae20856 T6-novisp
Abp53292 Synthetic
Aae20864 S7-novisp
Aae20871 S10-novis
Aae20878 S11-novis
Aae20857 S6-novisp
Aae20872 S10-novis
Aae20873 D10-novis
Aae20858 B6-novisp
Aae20866 D7-novisp
Aae20879 E11-novis
Aae20865 E7-novisp
Aae20880 D6-novisp
Aae20859 D5-novisp
Aae20862 G7-novisp
Aae20876 G11-novis
Aae20883 G10-novis
Aae20869 G10-novis
Aae20855 G6-novisp

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 49.9218 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-9

Sequence: 1 NLRRIKRIHIKRY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_03: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	62.0	160	1	SCS1_SHEEP
2	49	62.0	160	1	SCS2_SHEEP
3	48	60.8	500	1	TF3B_SCHPO
4	46	58.2	349	2	Q736DS
5	46	58.2	349	2	Q81P89
6	46	58.2	349	2	Q6HH12
7	45	57.0	308	2	Q8R2C7
8	45	57.0	402	2	Q81L43
9	45	57.0	834	2	Q7RR10
10	44	55.7	684	2	Q7GNN1
11	44	55.7	954	2	Q9GQ15
12	44	55.7	969	2	Q9U022
13	44	55.7	1137	2	Q6LF77
14	43.5	55.1	313	2	Q8CNR3
15	43	54.4	146	2	Q9A1H3
16	43	54.4	182	2	Q896E1
17	43	54.4	234	2	Q59264
18	43	54.4	250	2	Q6LF79
19	43	54.4	537	2	Q97W16
20	43	54.4	638	2	Q8D796
21	43	54.4	660	2	Q7W6A0
22	43	54.4	821	1	MCW6_HUMAN
23	43	54.4	840	2	Q9PHN4
24	43	54.4	875	2	Q8R8R4
25	43	54.4	878	2	Q7RY40
26	43	54.4	3267	2	Q81BZ0
27	42.5	53.8	301	2	Q7Q4C0
28	42	53.2	125	2	Q9AVZ1
29	42	53.2	146	1	RUVX MYCPU
30	42	53.2	198	2	Q6L1E8
31	42	53.2	231	2	Q8RAG4

ALIGNMENTS

32	42	53.2	233	2	Q9L7X2	Q9L7X2 clostridium
33	42	53.2	233	2	Q8XJ18	Q8XJ18 clostridium
34	42	53.2	234	2	Q95ZM1	Q95ZM1 caenorhabditis
35	42	53.2	420	1	PR11_HUMAN	P96642 homo sapien
36	42	53.2	460	2	Q9VJ03	Q9VJ03 drosophila
37	42	53.2	507	1	MCW6_RAT	Q62724 rattus norv
38	42	53.2	549	2	Q81PC2	Q81PC2 drosophila
39	42	53.2	581	2	Q6EBB6	Q6EBB6 campylobact
40	42	53.2	1279	2	Q81B12	Q81B12 plasmodium
41	42	53.2	2084	2	Q81LJ6	Q81LJ6 plasmodium
42	42	53.2	6077	2	Q6LPH6	Q6LPH6 plasmodium
43	41.5	52.5	313	2	Q8NVV6	Q8NVV6 staphylococ
44	41.5	52.5	313	2	Q53606	Q53606 staphylococ
45	41.5	52.5	313	2	Q7A2Q3	Q7A2Q3 staphylococ

RESULT 1
ID SCS1_SHEEP STANDARD; PRT; 160 AA.
AC P49928;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3; RA Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.; RT "Molecular analysis of the sheep cathelin family reveals a novel antimicrobial peptide.";
RT FEBS Lett. 377:519-522(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Huttner K.M., Mahoney M.M.; RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Thermostable, broad spectrum, bactericidal agent.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: X92757; CAA63412.1; -
DR EMBL: U60600; AAB49715.1; -
DR PDB: 1FRR; NMR; A=132-160.
DR InterPro: IPR001894; Cathelicidin.
DR Pfam: PF00666; Cathelicidins; 1.
DR PROSITE: PS001838; Cathelicidins; 1.
DR PROSITE: PS00946; CATHELICIDINS_1; 1.
DR PROSITE: PS00947; CATHELICIDINS_2; 1.
KW 3D-structure; Antibiotic; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 131
FT PEPTIDE 132 160
FT MOD_RES 30 30
FT FT
FT DISULFID 86 97
FT FT

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 9.92179 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-9

Perfect score: 79

Sequence: 1 NRRRIIRKIHIIKKY 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	62.0	152	2	S68411 cathelin-related p
2	49	62.0	160	2	S68412 cathelin-related p
3	49	62.0	160	2	S68228 myeloid antimicrob
4	43	54.4	234	2	D97108 DNA-dependent RNA
5	43	54.4	234	2	I40822 sigk protein - C1o
6	43	54.4	537	2	C90389 conserved hypochet
7	42	53.2	125	2	A99114 conserved hypochet
8	42	53.2	146	2	D90581 conserved hypochet
9	42	53.2	420	2	S45630 DNA primase chain
10	42	53.2	507	2	T10753 interstitial DNA rep
11	42	53.2	1741	2	T15978 hypochetrical prote
12	41.5	52.5	313	2	A89971 cmp-binding factor
13	41	51.9	41	2	S77768 hypochetrical prote
14	41	51.9	186	2	B90116 hypochetrical prote
15	41	51.9	337	2	S46010 hypochetrical prote
16	41	51.9	414	2	G64091 cell division prot
17	41	51.9	417	2	A33269 DNA primase (BC 2.
18	41	51.9	463	2	S75369 hypochetrical prote
19	41	51.9	613	2	F64056 probable ATP-depen
20	41	51.9	867	2	G69485 DNA-directed RNA p
21	40.5	51.3	381	1	C64416 conserved hypochet
22	40	50.6	105	2	F71128 hypochetrical prote
23	40	50.6	189	2	H96903 transcritption regu
24	40	50.6	370	2	C70464 GTP-binding protei
25	40	50.6	552	2	B90749 hypochetrical prote
26	40	50.6	552	2	F85599 hypochetrical prote
27	40	50.6	552	2	D64826 ybid protein - Bac
28	40	50.6	1634	2	B64410 DNA-directed RNA p
29	39	49.4	113	2	G90223 DNA-directed RNA p

30	39	49.4	156	1	D71689	hypothetical prote
31	39	49.4	202	1	H70318	conserved hypochet
32	39	49.4	210	2	AC1577	precursor isomeras
33	39	49.4	292	2	A97035	cation efflux syst
34	39	49.4	319	1	S19248	RNA-directed DNA p
35	39	49.4	334	2	B72301	endoglucanase - Th
36	39	49.4	391	2	B82360	cell division prot
37	39	49.4	407	2	T37888	hypothetical prote
38	39	49.4	483	2	B82160	hypothetical prote
39	39	49.4	762	2	S56141	HAKI protein - Yea
40	39	49.4	87	2	S00180	spermatid protein
41	38	48.1	102	2	AD1420	PTS celllobiose-spe
42	38	48.1	102	2	AE1795	PTS celllobiose-spe
43	38	48.1	172	2	T28288	ORF MSY127 hypothe
44	38	48.1	177	2	T28362	hypothetical prote
45	38	48.1	197	2	A90594	holliday junction

ALIGNMENTS

RESULT 1

S68411

cathelin-related protein 2 precursor - sheep (fragment)

C/Spectrum: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68411

R/Mahoney, M.M.; Lee, A.Y.; Brezniski-Calguri, D.J.; Huttner, K.M.

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411; MUID:96140581; PMID:8549789

A/Accession: S68411

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-152 <MAH>

A/Cross-references: EMBL:X92757

C/Genetics:

A/Gene: SC5-2

C/Superfamily: cathelin; cystatin homology

F/1-21/Domain: signal sequence #status predicted <SIG>

F/14-123/Domain: cystatin homology <CYS>

F/21-123/Domain: propeptide #status predicted <PRO>

F/124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match 62.0%; Score 49; DB 2; Length 152;

Best local similarity 66.7%; Pred. No. 1.4;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LRRRIIRKIHIIKKY 16

Db 126 LRRIRKIHIIKKY 140

RESULT 2

S68412

cathelin-related protein 1 precursor - sheep

C/Spectrum: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68412

R/Mahoney, M.M.; Lee, A.Y.; Brezniski-Calguri, D.J.; Huttner, K.M.

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411; MUID:96140581; PMID:8549789

A/Accession: S68412

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <MAH>

A/Cross-references: EMBL:X92758

C/Genetics:

A/Gene: SC5-1

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/22-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 43.5307 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-9

Sequence: 1 NLRRIKIHIIKKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	14	US-10-060-102-14
2	79	100.0	16	15	US-10-721-839-14
3	79	100.0	18	9	US-09-840-009-2
4	79	100.0	18	9	US-09-840-009-9
5	79	100.0	18	9	US-09-840-009-16
6	79	100.0	18	9	US-09-840-009-23
7	79	100.0	18	9	US-09-840-009-30
8	79	100.0	18	14	US-10-060-102-9
9	79	100.0	18	14	US-10-060-102-12
10	79	100.0	18	15	US-10-721-839-9
11	79	100.0	18	15	US-10-721-839-12
12	79	100.0	29	14	US-10-060-102-8
13	79	100.0	29	15	US-10-721-839-8

14	77	97.5	16	14	US-10-060-102-15	Sequence 15, Appl
15	77	97.5	16	15	US-10-721-839-15	Sequence 15, Appl
16	77	97.5	18	14	US-10-060-102-10	Sequence 11, Appl
17	77	97.5	18	14	US-10-060-102-11	Sequence 10, Appl
18	77	97.5	18	15	US-10-721-839-10	Sequence 11, Appl
19	77	97.5	18	15	US-10-721-839-11	Sequence 4, Appl1
20	74	93.7	18	9	US-09-840-009-4	Sequence 8, Appl1
21	74	93.7	18	9	US-09-840-009-8	Sequence 11, Appl
22	74	93.7	18	9	US-09-840-009-11	Sequence 15, Appl
23	74	93.7	18	9	US-09-840-009-15	Sequence 18, Appl
24	74	93.7	18	9	US-09-840-009-18	Sequence 22, Appl
25	74	93.7	18	9	US-09-840-009-22	Sequence 25, Appl
26	74	93.7	18	9	US-09-840-009-25	Sequence 29, Appl
27	74	93.7	18	14	US-10-060-102-25	Sequence 25, Appl
28	74	93.7	18	15	US-10-721-839-25	Sequence 5, Appl1
29	73	92.4	18	9	US-09-840-009-5	Sequence 12, Appl
30	73	92.4	18	9	US-09-840-009-12	Sequence 19, Appl
31	73	92.4	18	9	US-09-840-009-19	Sequence 26, Appl
32	73	92.4	18	9	US-09-840-009-26	Sequence 6, Appl1
33	72	91.1	18	9	US-09-840-009-6	Sequence 7, Appl1
34	72	91.1	18	9	US-09-840-009-7	Sequence 13, Appl
35	72	91.1	18	9	US-09-840-009-13	Sequence 14, Appl
36	72	91.1	18	9	US-09-840-009-14	Sequence 20, Appl
37	72	91.1	18	9	US-09-840-009-20	Sequence 21, Appl
38	72	91.1	18	9	US-09-840-009-21	Sequence 27, Appl
39	72	91.1	18	9	US-09-840-009-27	Sequence 28, Appl
40	72	91.1	18	9	US-09-840-009-28	Sequence 3, Appl1
41	72	91.1	18	9	US-09-840-009-3	Sequence 10, Appl
42	71	89.9	18	9	US-09-840-009-10	Sequence 17, Appl
43	71	89.9	18	9	US-09-840-009-17	Sequence 24, Appl
44	71	89.9	18	9	US-09-840-009-24	
45	71	89.9	18	9	US-09-840-009-24	

ALIGNMENTS

RESULT 1
US-10-060-102-14
; Sequence 14, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/305,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-14

Query Match 100.0%; Score 79; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 NLRRIKIHIIKKY 16

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 15.1955 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-9

Sequence: 1 NLRRIKIHIIKKY 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/5a_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	18	4	US-09-840-009-2
2	79	100.0	18	4	US-09-840-009-9
3	79	100.0	18	4	US-09-840-009-16
4	79	100.0	18	4	US-09-840-009-23
5	79	100.0	18	4	US-09-840-009-30
6	74	93.7	18	4	US-09-840-009-4
7	74	93.7	18	4	US-09-840-009-8
8	74	93.7	18	4	US-09-840-009-11
9	74	93.7	18	4	US-09-840-009-15
10	74	93.7	18	4	US-09-840-009-18
11	74	93.7	18	4	US-09-840-009-22
12	74	93.7	18	4	US-09-840-009-25
13	74	93.7	18	4	US-09-840-009-29
14	73	92.4	18	4	US-09-840-009-5
15	73	92.4	18	4	US-09-840-009-12
16	73	92.4	18	4	US-09-840-009-19
17	73	92.4	18	4	US-09-840-009-26
18	72	91.1	18	4	US-09-840-009-6
19	72	91.1	18	4	US-09-840-009-7
20	72	91.1	18	4	US-09-840-009-13
21	72	91.1	18	4	US-09-840-009-14
22	72	91.1	18	4	US-09-840-009-20
23	72	91.1	18	4	US-09-840-009-21
24	72	91.1	18	4	US-09-840-009-27
25	72	91.1	18	4	US-09-840-009-28
26	71	89.9	18	4	US-09-840-009-3
27	71	89.9	18	4	US-09-840-009-10

28	71	89.9	18	4	US-09-840-009-17	Sequence 17, Appl
29	71	89.9	18	4	US-09-840-009-24	Sequence 24, Appl
30	71	89.9	18	4	US-09-840-009-31	Sequence 31, Appl
31	65	82.3	18	4	US-09-840-009-34	Sequence 34, Appl
32	65	82.3	18	4	US-09-840-009-35	Sequence 35, Appl
33	63	79.7	18	4	US-09-840-009-32	Sequence 32, Appl
34	63	79.7	18	4	US-09-840-009-33	Sequence 33, Appl
35	59	74.7	18	4	US-09-840-009-1	Sequence 36, Appl
36	57	72.2	18	4	US-09-840-009-36	Sequence 37, Appl
37	57	72.2	18	4	US-09-840-009-37	Sequence 38, Appl
38	49	62.0	160	4	US-09-917-340-36	Sequence 39, Appl
39	45	57.0	169	4	US-09-270-767-35406	Sequence 40, Appl
40	45	57.0	169	4	US-09-270-767-50623	Sequence 41, Appl
41	44	55.7	205	3	US-09-134-001C-4766	Sequence 42, Appl
42	43.5	55.1	167	4	US-09-710-279-1502	Sequence 43, Appl
43	43.5	55.1	320	3	US-09-134-001C-1823	Sequence 44, Appl
44	54.4	54.4	823	4	US-09-949-016-8339	Sequence 45, Appl
45	42	53.2	526	4	US-09-270-767-45588	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match 100.0%; Score 79; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NLRRIKIHIIKKY 16
DB 2 NLRRIKIHIIKKY 17
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Alan J.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 56.0894 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-9

Perfect score: 79

Sequence: 1 NLRRIKRIHIIKKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	4	AAE20877
2	79	100.0	16	5	AAE20856
3	79	100.0	16	5	ABP53281
4	79	100.0	16	4	AAE20855
5	79	100.0	16	4	AAE20854
6	79	100.0	16	5	AAE20875
7	79	100.0	16	5	AAE20861
8	79	100.0	16	5	AAE20868
9	79	100.0	16	5	ABP53276
10	79	100.0	16	5	ABP53279
11	79	100.0	16	5	ABP53275
12	79	100.0	16	5	ABP53278
13	79	100.0	16	5	ABP53277
14	79	100.0	16	5	ABP53276
15	79	100.0	16	5	ABP53275
16	79	100.0	16	5	ABP53278
17	79	100.0	16	5	ABP53277
18	79	100.0	16	5	ABP53276
19	79	100.0	16	5	ABP53275
20	79	100.0	16	5	ABP53278
21	79	100.0	16	5	ABP53277
22	79	100.0	16	5	ABP53276
23	79	100.0	16	5	ABP53275
24	79	100.0	16	5	ABP53278
25	79	100.0	16	5	ABP53277

26	74	93.7	18	5	AAE20877	AAE20877 T11-novis
27	74	93.7	18	5	AAE20856	AAE20856 T6-novisp
28	74	93.7	18	5	ABP53292	ABP53292 Synthetic
29	73	92.4	18	5	AAE20864	AAE20864 S7-novisp
30	73	92.4	18	5	AAE20871	AAE20871 S10-novis
31	73	92.4	18	5	AAE20878	AAE20878 S11-novis
32	73	92.4	18	5	AAE20857	AAE20857 S6-novisp
33	72	91.1	18	5	AAE20872	AAE20872 E10-novis
34	72	91.1	18	5	AAE20873	AAE20873 D10-novis
35	72	91.1	18	5	AAE20858	AAE20858 E6-novisp
36	72	91.1	18	5	AAE20865	AAE20865 D7-novisp
37	72	91.1	18	5	AAE20879	AAE20879 E7-novisp
38	72	91.1	18	5	AAE20880	AAE20880 E7-novisp
39	72	91.1	18	5	AAE20859	AAE20859 D6-novisp
40	72	91.1	18	5	AAE20862	AAE20862 G7-novisp
41	71	89.9	18	5	AAE20876	AAE20876 G11-novis
42	71	89.9	18	5	AAE20883	AAE20883 G10-novis
43	71	89.9	18	5	AAE20869	AAE20869 G10-novis
44	71	89.9	18	5	AAE20855	AAE20855 G6-novisp
45	71	89.9	18	5	AAE20855	AAE20855 G6-novisp

ALIGNMENTS

RESULT 1

AAE20856 standard; peptide; 16 AA.

AAE20856;

15-MAY-2001 (first entry)

Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:9.

Ovine: SNAP29; lupine: RCAP 18; cathelicidin; antimicrobial;

bactericidal; antibiotic; antiviral; microbial growth inhibitor;

proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

Burkholderia cepacia; Alcaligenes; Xanthomonas.

Ovis aries.

WO200112668-A1.

22-FEB-2001.

18-AUG-2000; 2000WO-US022781.

18-AUG-1999; 99US-0149886P.

(IOWA) UNIV IOWA RES FOUND.

(REGC) UNIV CALIFORNIA.

Tack BE, McCreary P, Welsh M, Travis SM, Lehrer R;

WPI; 2001-234911/24.

New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections.

Claim 1; Page 103; 137p; English.

AAE20848 to AAE20875 represent antimicrobial peptides (I), of which AAE20848 to AAE20864, AAE20867 and AAE20875 are derived from the ovine SNAP 29 cathelicidin family peptide, and AAE20865 to AAE20873 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antimicrobial and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (II) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 56.162 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-8

Perfect score: 90

Sequence: 1 KMLRRIRKIIHIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	63.3	160	1	SCS1_SHEEP
2	57	63.3	160	1	SCS2_SHEEP
3	54	60.0	146	2	O9A1H3
4	50	55.6	255	2	O9LJW2
5	49	54.4	581	2	O6RBB6
6	48	53.3	250	2	O6LFP79
7	48	53.3	500	1	TF3B_SCHPO
8	48	53.3	3267	2	O81B20
9	47	52.2	113	2	O70320
10	47	52.2	2017	2	O675T1
11	46.5	51.7	314	2	O651T6
12	46.5	51.7	324	2	O62X75
13	46	51.1	282	2	O8DYR3
14	46	51.1	282	2	O8B4C0
15	46	51.1	319	2	O05804
16	46	51.1	349	2	O736D5
17	46	51.1	349	2	O81P89
18	46	51.1	349	2	O6H1I2
19	46	51.1	684	2	O70NN1
20	46	51.1	954	2	O9GQI5
21	46	51.1	969	2	O9U022
22	45.5	50.6	381	1	TH11_METJA
23	45	50.0	332	2	O82MTO
24	45	50.0	308	2	O8R2C7
25	45	50.0	402	2	O81L43
26	45	50.0	834	2	O7RR10
27	45	50.0	1634	1	DPOL_METJA
28	44	48.9	78	2	O8ZYK7
29	44	48.9	93	2	O64ID6
30	44	48.9	124	2	O649W3
31	44	48.9	125	2	O64EAS

ALIGNMENTS

32	44	48.9	219	2	O6FP91	O6FB91 acinetobact
33	44	48.9	291	2	O738Z6	O738Z6 bacillus ce
34	44	48.9	301	2	O6H2B4	O6H2B4 bacillus ce
35	44	48.9	301	2	O63BX5	O63BX5 bacillus ce
36	44	48.9	301	2	O81E24	O81E24 bacillus ce
37	44	48.9	301	2	O6H2E6	O6H2E6 bacillus th
38	44	48.9	303	2	O81R41	O81R41 bacillus an
39	44	48.9	343	2	O76C22	O76C22 pyrococcus
40	44	48.9	756	2	O93XR9	O93XR9 bruniera g
41	44	48.9	807	1	H1S8_PHOHL	O7N611 photorhabd
42	44	48.9	840	2	O9DHN4	O9DHN4 yaba-like d
43	44	48.9	1043	2	O81B28	O81B28 plasmodium
44	44	48.9	1137	2	O6LF77	O6LF77 plasmodium
45	44	48.9	1401	1	DP03_THETN	O8ra32 thermoaer

RESULT 1
ID SCS1_SHEEP STANDARD; PRT; 160 AA.
AC P49928;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SMAP-29).
DE 29) (Myeloid antibacterial peptide SMAP-29).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NC NCB1_Taxid=9940;
RN [1]
RP TISSUE=bone marrow;
RC TISSUE=bone marrow;
RX MEDLINE=86140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RA Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;
RT "Molecular analysis of the sheep cathelin family reveals a novel
antimicrobial peptide.";
RL FEBS Lett. 377:519-522(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Huttner K.M., Mahoney M.M.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Thermostable, broad spectrum, bactericidal agent.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X92757; CA63412.1; -;
DR EMBL; U60600; AAB49715.1; -;
DR PDB; 1PRY; NMR; A=132-160.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR PROSITE; PS001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW 3D-structure; Antibiotic; Pyrolydine carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 131
FT PEPTIDE 132 160
FT MOD_RSS 30 30
FT FT
FT DSUFID 86 97
By similarity.
By similarity.
Cathelin-related peptide SCS.
Pyrolydine carboxylic acid (By
similarity).
By similarity.

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OM protein - protein search, using SW model

Run on: May 2, 2005, 13:03:56 ; Search time 48.9721 Seconds
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-8

Perfect score: 90

Sequence: 1 KMLRRIIRKIIHIKKYG 18

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

1426032

Total number of hits satisfying chosen parameters:

1426032

Minimum DB seq length: 0

1426032

Maximum DB seq length: 2000000000

1426032

Post-Processing: Minimum Match 0%

1426032

Maximum Match 100%

1426032

Listing first 45 summaries

1426032

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubppa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PTCT_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	90	100.0	18	9	US-09-840-009-9
3	90	100.0	18	9	US-09-840-009-16
4	90	100.0	18	9	US-09-840-009-23
5	90	100.0	18	9	US-09-840-009-30
6	90	100.0	18	14	US-10-060-102-9
7	90	100.0	18	14	US-10-060-102-12
8	90	100.0	18	15	US-10-721-839-9
9	90	100.0	18	15	US-10-721-839-12
10	90	100.0	29	14	US-10-060-102-8
11	90	100.0	29	15	US-10-721-839-8
12	88	97.8	18	14	US-10-060-102-10
13	88	97.8	18	14	US-10-060-102-11

14	88	97.8	18	15	US-10-721-839-10	Sequence 10, Appl
15	88	97.8	18	15	US-10-721-839-11	Sequence 11, Appl
16	85	94.4	18	9	US-09-840-009-4	Sequence 4, Appl
17	85	94.4	18	9	US-09-840-009-8	Sequence 8, Appl
18	85	94.4	18	9	US-09-840-009-11	Sequence 11, Appl
19	85	94.4	18	9	US-09-840-009-15	Sequence 15, Appl
20	85	94.4	18	9	US-09-840-009-18	Sequence 18, Appl
21	85	94.4	18	9	US-09-840-009-22	Sequence 22, Appl
22	85	94.4	18	9	US-09-840-009-25	Sequence 25, Appl
23	85	94.4	18	9	US-09-840-009-29	Sequence 29, Appl
24	85	94.4	18	14	US-10-060-102-25	Sequence 25, Appl
25	85	94.4	18	15	US-10-721-839-25	Sequence 25, Appl
26	84	93.3	18	9	US-09-840-009-5	Sequence 5, Appl
27	84	93.3	18	9	US-09-840-009-12	Sequence 12, Appl
28	84	93.3	18	9	US-09-840-009-19	Sequence 19, Appl
29	84	93.3	18	9	US-09-840-009-26	Sequence 26, Appl
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36	83	92.2	18	9	US-09-840-009-27	Sequence 27, Appl
37	83	92.2	18	9	US-09-840-009-28	Sequence 28, Appl
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43	82	91.1	18	14	US-10-060-102-26	Sequence 26, Appl
44	82	91.1	18	14	US-10-077-624-17	Sequence 17, Appl
45	82	91.1	18	15	US-10-721-839-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. US20020082195A1
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840-009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 KMLRRIIRKIIHIKKYG 18
RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 17.095 Seconds

(without alignments)
78,601 Million cell updates/sec

Title: US-09-642-744d-8

Sequence: 1 KNLRRIRKIRHIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74643064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	18	4	US-09-840-009-2
2	90	100.0	18	4	US-09-840-009-9
3	90	100.0	18	4	US-09-840-009-16
4	90	100.0	18	4	US-09-840-009-23
5	90	100.0	18	4	US-09-840-009-30
6	85	94.4	18	4	US-09-840-009-4
7	85	94.4	18	4	US-09-840-009-8
8	85	94.4	18	4	US-09-840-009-11
9	85	94.4	18	4	US-09-840-009-15
10	85	94.4	18	4	US-09-840-009-18
11	85	94.4	18	4	US-09-840-009-22
12	85	94.4	18	4	US-09-840-009-25
13	85	94.4	18	4	US-09-840-009-29
14	84	93.3	18	4	US-09-840-009-5
15	84	93.3	18	4	US-09-840-009-12
16	84	93.3	18	4	US-09-840-009-19
17	84	93.3	18	4	US-09-840-009-26
18	83	92.2	18	4	US-09-840-009-6
19	83	92.2	18	4	US-09-840-009-7
20	83	92.2	18	4	US-09-840-009-13
21	83	92.2	18	4	US-09-840-009-14
22	83	92.2	18	4	US-09-840-009-20
23	83	92.2	18	4	US-09-840-009-21
24	83	92.2	18	4	US-09-840-009-27
25	83	92.2	18	4	US-09-840-009-28
26	82	91.1	18	4	US-09-840-009-3
27	82	91.1	18	4	US-09-840-009-10

28	82	91.1	18	4	US-09-840-009-17	Sequence 17, Appl
29	82	91.1	18	4	US-09-840-009-24	Sequence 24, Appl
30	82	91.1	18	4	US-09-840-009-31	Sequence 31, Appl
31	76	84.4	18	4	US-09-840-009-34	Sequence 34, Appl
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33	74	82.2	18	4	US-09-840-009-32	Sequence 32, Appl
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ALIGNMENTS

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RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          100.0%; Score 90; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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CC *Pseudomonas aeruginosa*, *Burkholderia cepacia*, *Alcaligenes* and *Xanthomonas*